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C12P 19/18 (2006.01)(72) Inventors: **YOUGEN LI**, PENNINGTON, NJ (US); **ELLEN D. SEMKE**, NEWARK, DE (US); **MARK S. PAYNE**, WILMINGTON, DE (US); **JARED B. PARKER**, ELKTON, MD (US); **SUSAN MARIE HENNESSEY**, AVONDALE, PA (US); **SLAVKO KRALJ**, COPENHAGEN K (DK); **VELI ALKAN**, PALO ALTO, CA (US); **RICHARD BOTT**, PALO ALTO, CA (US)(52) **U.S. Cl.**
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(60) Provisional application No. 62/557,834, filed on Sep. 13, 2017.

(57) **ABSTRACT**

Disclosed herein are glucosyltransferases with modified amino acid sequences. Such engineered enzymes synthesize alpha-glucan products having increased molecular weight. Further disclosed are reactions and methods in which engineered glucosyltransferases are used to produce alpha-glucan.

Specification includes a Sequence Listing.

ENGINEERED GLUCOSYLTRANSFERASES

[0001] This application claims the benefit of U.S. Provisional Application No. 62/557,834 (filed Sep. 13, 2017), which is incorporated herein by reference in its entirety.

FIELD

[0002] The present disclosure is in the field of enzyme catalysis. For example, the disclosure pertains to glucosyltransferase enzymes with modified amino acid sequences. Such modified enzymes synthesize products with increased molecular weight.

REFERENCE TO SEQUENCE LISTING SUBMITTED ELECTRONICALLY

[0003] The official copy of the sequence listing is submitted electronically via EFS-Web as an ASCII formatted sequence listing with a file named 20180911_CL6159WOPCT_SequenceListing_ST25 created on Sep. 11, 2018, and having a size of about 315 kilobytes and is filed concurrently with the specification. The sequence listing contained in this ASCII-formatted document is part of the specification and is herein incorporated by reference in its entirety.

BACKGROUND

[0004] Driven by a desire to use polysaccharides in various applications, researchers have explored for polysaccharides that are biodegradable and that can be made economically from renewably sourced feedstocks. One such polysaccharide is alpha-1,3-glucan, an insoluble glucan polymer characterized by having alpha-1,3-glycosidic linkages. This polymer has been prepared, for example, using a glucosyltransferase enzyme isolated from *Streptococcus salivarius* (Simpson et al., *Microbiology* 141:1451-1460, 1995). Also for example, U.S. Pat. No. 7,000,000 disclosed the preparation of a spun fiber from enzymatically produced alpha-1,3-glucan. Various other glucan materials have also been studied for developing new or enhanced applications. For example, U.S. Patent Appl. Publ. No. 2015/0232819 discloses enzymatic synthesis of several insoluble glucans having mixed alpha-1,3 and -1,6 linkages.

[0005] While these and other advances have been made in producing glucan polymers using glucosyltransferase enzymes, less attention appears to have been drawn to enhancing the molecular weight of insoluble glucan products synthesized by such enzymes. Addressing this technological gap, disclosed herein are glucosyltransferases with modified amino acid sequences that produce higher molecular weight insoluble glucan products.

SUMMARY

[0006] In one embodiment, the present disclosure concerns a non-native glucosyltransferase comprising at least one amino acid substitution at a position corresponding with

amino acid residue Asn-531, Arg-534, Thr-563, Glu-567, Val-586, Gln-588, Ile-591, Lys-593, Ile-608, Ala-610, Leu-661, Arg-722, Thr-728, Met-732, Arg-741, Asn-743, Ala-777, Tyr-848, or Ile-1453 of SEQ ID NO:62, wherein the non-native glucosyltransferase synthesizes insoluble alpha-glucan comprising 1,3-linkages, and the molecular weight of the insoluble alpha-glucan is higher than the molecular weight of insoluble alpha-glucan synthesized by a second glucosyltransferase that only differs from the non-native glucosyltransferase at the substitution position(s).

[0007] In another embodiment, the present disclosure concerns a polynucleotide comprising a nucleotide sequence encoding a non-native glucosyltransferase as presently disclosed, optionally wherein one or more regulatory sequences are operably linked to the nucleotide sequence, and preferably wherein the one or more regulatory sequences include a promoter sequence.

[0008] In another embodiment, the present disclosure concerns a reaction composition comprising water, sucrose, and a non-native glucosyltransferase as presently disclosed.

[0009] In another embodiment, the present disclosure concerns a method of producing insoluble alpha-glucan comprising: (a) contacting at least water, sucrose, and a non-native glucosyltransferase enzyme as presently disclosed, whereby insoluble alpha-glucan is produced; and (b) optionally, isolating the insoluble alpha-glucan produced in step (a).

[0010] In another embodiment, the present disclosure concerns a method of preparing a polynucleotide sequence encoding a non-native glucosyltransferase, the method comprising: (a) identifying a polynucleotide sequence encoding a parent glucosyltransferase that (i) comprises an amino acid sequence that is at least about 40% identical to SEQ ID NO:4 or positions 55-960 of SEQ ID NO:4, and (ii) synthesizes insoluble alpha-glucan comprising 1,3-linkages; and (b) modifying the polynucleotide sequence identified in step (a) to substitute at least one amino acid of the parent glucosyltransferase at a position corresponding with amino acid residue Asn-531, Arg-534, Thr-563, Glu-567, Val-586, Gln-588, Ile-591, Lys-593, Ile-608, Ala-610, Leu-661, Arg-722, Thr-728, Met-732, Arg-741, Asn-743, Ala-777, Tyr-848, or Ile-1453 of SEQ ID NO:62, thereby providing a polynucleotide sequence encoding a non-native glucosyltransferase that synthesizes insoluble alpha-glucan with a molecular weight that is higher than the molecular weight of insoluble alpha-glucan synthesized by the parent glucosyltransferase.

BRIEF DESCRIPTION OF THE SEQUENCES

[0011]

TABLE 1

Summary of Nucleic Acid and Protein SEQ ID Numbers ^b		
Description	Nucleic acid SEQ ID NO.	Protein SEQ ID NO.
GTF 0874, <i>Streptococcus sobrinus</i> . The first 156 amino acids of the protein are deleted compared to GENBANK Identification No. 450874; a start methionine is included.	1 ^a	2 (1435 aa)

TABLE 1-continued

Summary of Nucleic Acid and Protein SEQ ID Numbers ^b		
Description	Nucleic acid SEQ ID NO.	Protein SEQ ID NO.
GTF 6855, <i>Streptococcus salivarius</i> SK126. The first 178 amino acids of the protein are deleted compared to GENBANK Identification No. 228476855 (Acc. No. ZP_04061500.1); a start methionine is included.	3 ^a	4 (1341 aa)
GTF 2379, <i>Streptococcus salivarius</i> . The first 203 amino acids of the protein are deleted compared to GENBANK Identification No. 662379; a start methionine is included.	5 ^a	6 (1247 aa)
GTF 7527 or GTFJ, <i>Streptococcus salivarius</i> . The first 42 amino acids of the protein are deleted compared to GENBANK Identification No. 47527; a start methionine is included.	7 ^a	8 (1477 aa)
GTF 1724, <i>Streptococcus downei</i> . The first 162 amino acids of the protein are deleted compared to GENBANK Identification No. 121724; a start methionine is included.	9 ^a	10 (1436 aa)
GTF 0544, <i>Streptococcus mutans</i> . The first 164 amino acids of the protein are deleted compared to GENBANK Identification No. 290580544; a start methionine is included.	11 ^a	12 (1313 aa)
GTF 5926, <i>Streptococcus dentirousei</i> . The first 144 amino acids of the protein are deleted compared to GENBANK Identification No. 167735926; a start methionine is included.	13 ^a	14 (1323 aa)
GTF 4297, <i>Streptococcus oralis</i> . The first 228 amino acids of the protein are deleted compared to GENBANK Identification No. 7684297; a start methionine is included.	15 ^a	16 (1348 aa)
GTF 5618, <i>Streptococcus sanguinis</i> . The first 223 amino acids of the protein are deleted compared to GENBANK Identification No. 328945618; a start methionine is included.	17 ^a	18 (1348 aa)
GTF 2765, unknown <i>Streptococcus</i> sp. C150. The first 193 amino acids of the protein are deleted compared to GENBANK Identification No. 322372765; a start methionine is included.	19 ^a	20 (1340 aa)
GTF 0427, <i>Streptococcus sobrinus</i> . The first 156 amino acids of the protein are deleted compared to GENBANK Identification No. 940427; a start methionine is included.	25 ^a	26 (1435 aa)
GTF 2919, <i>Streptococcus salivarius</i> PS4. The first 92 amino acids of the protein are deleted compared to GENBANK Identification No. 383282919; a start methionine is included.	27 ^a	28 (1340 aa)
GTF 2678, <i>Streptococcus salivarius</i> K12. The first 188 amino acids of the protein are deleted compared to GENBANK Identification No. 400182678; a start methionine is included.	29 ^a	30 (1341 aa)
GTF 3929, <i>Streptococcus salivarius</i> JIM8777. The first 178 amino acids of the protein are deleted compared to GENBANK Identification No. 387783929; a start methionine is included.	33 ^a	34 (1341 aa)
GTF 3298, <i>Streptococcus</i> sp. C150. The first 209 amino acids of the protein are deleted compared to GENBANK Identification No. 322373298; a start methionine is included.		59 (1242 aa)
Wild type GTFJ, <i>Streptococcus salivarius</i> . GENBANK Identification No. 47527.		60 (1518 aa)
Wild type GTF corresponding to GTF 2678, <i>Streptococcus salivarius</i> K12.		61 (1528 aa)
Wild type GTF corresponding to GTF 6855, <i>Streptococcus salivarius</i> SK126.		62 (1518 aa)
Wild type GTF corresponding to GTF 2919, <i>Streptococcus salivarius</i> PS4.		63 (1431 aa)
Wild type GTF corresponding to GTF 2765, unknown <i>Streptococcus</i> sp. C150.		64 (1532 aa)
Shorter version of GTF 7527, <i>Streptococcus salivarius</i> , (also referred to as “7527-NT” herein. The first 178 amino acids of the protein are deleted compared to GENBANK Identification No. 47527; a start methionine is included.		65 (1341 aa)
Terminator sequence added to pHY300PLK to derive the pHYT vector.	67	

^aThis DNA coding sequence is codon-optimized for expression in *E. coli*, and is merely disclosed as an example of a suitable coding sequence.

^bSEQ ID NOs: 21-24, 31, 32, 35-58 and 66 are intentionally not included in this table and merely serve as placeholders.

DETAILED DESCRIPTION

[0012] The disclosures of all cited patent and non-patent literature are incorporated herein by reference in their entirety.

[0013] Unless otherwise disclosed, the terms “a” and “an” as used herein are intended to encompass one or more (i.e., at least one) of a referenced feature.

[0014] Where present, all ranges are inclusive and combinable, except as otherwise noted. For example, when a range of “1 to 5” is recited, the recited range should be construed as including ranges “1 to 4”, “1 to 3”, “1-2”, “1-2 & 4-5”, “1-3 & 5”, and the like.

[0015] The terms “alpha-glucan”, “alpha-glucan polymer” and the like are used interchangeably herein. An alpha-glucan is a polymer comprising glucose monomeric units linked together by alpha-glycosidic linkages. In typical embodiments, an alpha-glucan herein comprises at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 100% alpha-glycosidic linkages. Examples of alpha-glucan polymers herein include alpha-1,3-glucan.

[0016] The terms “poly alpha-1,3-glucan”, “alpha-1,3-glucan”, “alpha-1,3-glucan polymer” and the like are used interchangeably herein. Alpha-1,3-glucan is a polymer comprising glucose monomeric units linked together by glycosidic linkages, typically wherein at least about 50% of the glycosidic linkages are alpha-1,3. Alpha-1,3-glucan in certain embodiments comprises at least 90% or 95% alpha-1,3 glycosidic linkages. Most or all of the other linkages in alpha-1,3-glucan herein typically are alpha-1,6, though some linkages may also be alpha-1,2 and/or alpha-1,4.

[0017] The terms “glycosidic linkage”, “glycosidic bond”, “linkage” and the like are used interchangeably herein and refer to the covalent bond that joins a carbohydrate (sugar) molecule to another group such as another carbohydrate. The term “alpha-1,3-glycosidic linkage” as used herein refers to the type of covalent bond that joins alpha-D-glucose molecules to each other through carbons 1 and 3 on adjacent alpha-D-glucose rings. The term “alpha-1,6-glycosidic linkage” as used herein refers to the covalent bond that joins alpha-D-glucose molecules to each other through carbons 1 and 6 on adjacent alpha-D-glucose rings. The glycosidic linkages of a glucan polymer herein can also be referred to as “glucosidic linkages”. Herein, “alpha-D-glucose” will be referred to as “glucose”.

[0018] The glycosidic linkage profile of an alpha-glucan herein can be determined using any method known in the art. For example, a linkage profile can be determined using methods using nuclear magnetic resonance (NMR) spectroscopy (e.g., ^{13}C NMR or ^1H NMR). These and other methods that can be used are disclosed in, for example, *Food Carbohydrates: Chemistry, Physical Properties, and Applications* (S. W. Cui, Ed., Chapter 3, S. W. Cui, Structural Analysis of Polysaccharides, Taylor & Francis Group LLC, Boca Raton, Fla., 2005), which is incorporated herein by reference.

[0019] The “molecular weight” of large alpha-glucan polymers herein can be represented as weight-average molecular weight (Mw) or number-average molecular weight (Mn), the units of which are in Daltons or grams/mole. Alternatively, the molecular weight of large alpha-glucan polymers can be represented as DP_w (weight average degree of polymerization) or DP_n (number average degree of polymerization). The molecular weight of smaller alpha-

glucan polymers such as oligosaccharides typically can be provided as “DP” (degree of polymerization), which simply refers to the number of glucoses comprised within the alpha-glucan. Various means are known in the art for calculating these various molecular weight measurements such as with high-pressure liquid chromatography (HPLC), size exclusion chromatography (SEC), or gel permeation chromatography (GPC).

[0020] The term “sucrose” herein refers to a non-reducing disaccharide composed of an alpha-D-glucose molecule and a beta-D-fructose molecule linked by an alpha-1,2-glycosidic bond. Sucrose is known commonly as table sugar.

[0021] The terms “leucrose” and “D-glucopyranosyl-alpha(1-5)-D-fructopyranose” are used interchangeably herein and refer to a disaccharide containing an alpha-1,5 glucosyl-fructose linkage.

[0022] The terms “glucosyltransferase”, “glucosyltransferase enzyme”, “GTF”, “glucansucrase” and the like are used interchangeably herein. The activity of a glucosyltransferase herein catalyzes the reaction of the substrate sucrose to make the products alpha-glucan and fructose. Other products (by-products) of a GTF reaction can include glucose, various soluble gluco-oligosaccharides, and leucrose. Wild type forms of glucosyltransferase enzymes generally contain (in the N-terminal to C-terminal direction) a signal peptide (which is typically removed by cleavage processes), a variable domain, a catalytic domain, and a glucan-binding domain. A glucosyltransferase herein is classified under the glycoside hydrolase family 70 (GH70) according to the CAZy (Carbohydrate-Active EnZymes) database (Cantarel et al., *Nucleic Acids Res.* 37:D233-238, 2009).

[0023] The term “glucosyltransferase catalytic domain” herein refers to the domain of a glucosyltransferase enzyme that provides alpha-glucan-synthesizing activity to a glucosyltransferase enzyme. A glucosyltransferase catalytic domain typically does not require the presence of any other domains to have this activity.

[0024] The terms “enzymatic reaction”, “glucosyltransferase reaction”, “glucan synthesis reaction”, “reaction composition”, “reaction formulation” and the like are used interchangeably herein and generally refer to a reaction that initially comprises water, sucrose, at least one active glucosyltransferase enzyme, and optionally other components. Components that can be further present in a glucosyltransferase reaction typically after it has commenced include fructose, glucose, leucrose, soluble gluco-oligosaccharides (e.g., DP2-DP7) (such may be considered as products or by-products, depending on the glucosyltransferase used), and/or insoluble alpha-glucan product(s) of DP8 or higher (e.g., DP100 and higher). It would be understood that certain glucan products, such as alpha-1,3-glucan with a degree of polymerization (DP) of at least 8 or 9, are water-insoluble and thus not dissolved in a glucan synthesis reaction, but rather may be present out of solution (e.g., by virtue of having precipitated from the reaction). It is in a glucan synthesis reaction where the step of contacting water, sucrose and a glucosyltransferase enzyme is performed. The term “under suitable reaction conditions” as used herein refers to reaction conditions that support conversion of sucrose to alpha-glucan product(s) via glucosyltransferase enzyme activity.

[0025] The terms “percent by volume”, “volume percent”, “vol %”, “v/v %” and the like are used interchangeably

herein. The percent by volume of a solute in a solution can be determined using the formula: [(volume of solute)/(volume of solution)] $\times$ 100%.

[0026] The terms “percent by weight”, “weight percentage (wt %)”, “weight-weight percentage (% w/w)” and the like are used interchangeably herein. Percent by weight refers to the percentage of a material on a mass basis as it is comprised in a composition, mixture, or solution.

[0027] The terms “aqueous conditions”, “aqueous reaction conditions”, “aqueous setting”, “aqueous system” and the like are used interchangeably herein. Aqueous conditions herein refer to a solution or mixture in which the solvent is at least about 60 wt % water, for example. A glucosyltransferase reaction herein is performed under aqueous conditions.

[0028] The terms “soluble”, “aqueous-soluble”, “water-soluble” and the like as used herein characterize a glucan that has the capability of dissolving in water and/or an aqueous solution herein. Examples of soluble glucans herein are certain oligosaccharides, such as alpha-1,3-glucan with a DP less than 8. In contrast, a glucan that is “insoluble”, “aqueous-insoluble”, “water-insoluble” (and like terms) does not dissolve (or does not appreciably dissolve) in water and/or an aqueous solution herein. Optionally, the conditions for determining solubility include a water/solution temperature range of about 1 to 85° C. (e.g., 20-25° C.) and/or a pH range of about 4-9 (e.g., 6-8).

[0029] The terms “polynucleotide”, “polynucleotide sequence”, “nucleic acid molecule” and the like are used interchangeably herein. These terms encompass nucleotide sequences and the like. A polynucleotide may be a polymer of DNA or RNA that is single- or double-stranded, that optionally contains synthetic, non-natural or altered nucleotide bases. A polynucleotide may be comprised of one or more segments of cDNA, genomic DNA, synthetic DNA, or mixtures thereof.

[0030] The term “gene” as used herein refers to a DNA polynucleotide sequence that expresses an RNA (RNA is transcribed from the DNA polynucleotide sequence) from a coding region, which RNA can be a messenger RNA (encoding a protein) or a non-protein-coding RNA. A gene may refer to the coding region alone, or may include regulatory sequences upstream and/or downstream to the coding region (e.g., promoters, 5'-untranslated regions, 3'-transcription terminator regions). A coding region encoding a protein can alternatively be referred to herein as an “open reading frame” (ORF). A gene that is “native” or “endogenous” refers to a gene as found in nature with its own regulatory sequences; such a gene is located in its natural location in the genome of a host cell. A “chimeric” gene refers to any gene that is not a native gene, comprising regulatory and coding sequences that are not found together in nature (i.e., the regulatory and coding regions are heterologous with each other). Accordingly, a chimeric gene may comprise regulatory sequences and coding sequences that are derived from different sources, or regulatory sequences and coding sequences derived from the same source, but arranged in a manner different than that found in nature. A “foreign” or “heterologous” gene can refer to a gene that is introduced into the host organism by gene transfer. Foreign/heterologous genes can comprise native genes inserted into a non-native organism, native genes introduced into a new location within the native host, or chimeric genes. Polynucleotide sequences in certain embodiments disclosed herein are het-

erologous. A “transgene” is a gene that has been introduced into the genome by a gene delivery procedure (e.g., transformation). A “codon-optimized” open reading frame has its frequency of codon usage designed to mimic the frequency of preferred codon usage of the host cell.

[0031] As used herein, the term “polypeptide” is defined as a chain of amino acid residues, usually having a defined sequence. As used herein the term polypeptide is interchangeable with the terms “peptides” and “proteins”. Typical amino acids contained in polypeptides herein include (respective three- and one-letter codes shown parenthetically): alanine (Ala, A), arginine (Arg, R), asparagine (Asn, N), aspartic acid (Asp, D), cysteine (Cys, C), glutamic acid (Glu, E), glutamine (Gln, Q), glycine (Gly, G), histidine (His, H), isoleucine (Ile, I), leucine (Leu, L), lysine (Lys, K), methionine (Met, M), phenylalanine (Phe, F), proline (Pro, P), serine (Ser, S), threonine (Thr, T), tryptophan (Trp, W), tyrosine (Tyr, Y), valine (Val, V).

[0032] The term “heterologous” means not naturally found in the location of interest. For example, a heterologous gene can be one that is not naturally found in a host organism, but that is introduced into the host organism by gene transfer. As another example, a nucleic acid molecule that is present in a chimeric gene can be characterized as being heterologous, as such a nucleic acid molecule is not naturally associated with the other segments of the chimeric gene (e.g., a promoter can be heterologous to a coding sequence).

[0033] A “non-native” amino acid sequence or polynucleotide sequence comprised in a cell or organism herein does not occur in a native (natural) counterpart of such cell or organism. Such an amino acid sequence or polynucleotide sequence can also be referred to as being heterologous to the cell or organism.

[0034] “Regulatory sequences” as used herein refer to nucleotide sequences located upstream of a gene’s transcription start site (e.g., promoter), 5' untranslated regions, introns, and 3' non-coding regions, and which may influence the transcription, processing or stability, and/or translation of an RNA transcribed from the gene. Regulatory sequences herein may include promoters, enhancers, silencers, 5' untranslated leader sequences, introns, polyadenylation recognition sequences, RNA processing sites, effector binding sites, stem-loop structures, and other elements involved in regulation of gene expression. One or more regulatory elements herein may be heterologous to a coding region herein.

[0035] A “promoter” as used herein refers to a DNA sequence capable of controlling the transcription of RNA from a gene. In general, a promoter sequence is upstream of the transcription start site of a gene. Promoters may be derived in their entirety from a native gene, or be composed of different elements derived from different promoters found in nature, or even comprise synthetic DNA segments. Promoters that cause a gene to be expressed in a cell at most times under all circumstances are commonly referred to as “constitutive promoters”. A promoter may alternatively be inducible. One or more promoters herein may be heterologous to a coding region herein.

[0036] A “strong promoter” as used herein refers to a promoter that can direct a relatively large number of productive initiations per unit time, and/or is a promoter driving a higher level of gene transcription than the average transcription level of the genes in a cell.

[0037] The terms “3' non-coding sequence”, “transcription terminator”, “terminator” and the like as used herein refer to DNA sequences located downstream of a coding sequence. This includes polyadenylation recognition sequences and other sequences encoding regulatory signals capable of affecting mRNA processing or gene expression.

[0038] As used herein, a first nucleic acid sequence is “hybridizable” to a second nucleic acid sequence when a single-stranded form of the first nucleic acid sequence can anneal to the second nucleic acid sequence under suitable annealing conditions (e.g., temperature, solution ionic strength). Hybridization and washing conditions are well known and exemplified in Sambrook J, Fritsch E F and Maniatis T, *Molecular Cloning: A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory: Cold Spring Harbor, N.Y. (1989), which is incorporated herein by reference, particularly Chapter 11 and Table 11.1.

[0039] The term “DNA manipulation technique” refers to any technique in which the sequence of a DNA polynucleotide sequence is modified. Although the DNA polynucleotide sequence being modified can be used as a substrate itself for modification, it does not have to be physically in hand for certain techniques (e.g., a sequence stored in a computer can be used as the basis for the manipulation technique). A DNA manipulation technique can be used to delete and/or mutate one or more DNA sequences in a longer sequence. Examples of a DNA manipulation technique include recombinant DNA techniques (restriction and ligation, molecular cloning), polymerase chain reaction (PCR), and synthetic DNA methods (e.g., oligonucleotide synthesis and ligation). Regarding synthetic DNA techniques, a DNA manipulation technique can entail observing a DNA polynucleotide in silico, determining desired modifications (e.g., one or more deletions) of the DNA polynucleotide, and synthesizing a DNA polynucleotide that contains the desired modifications.

[0040] The term “in silico” herein means in or on an information storage and/or processing device such as a computer; done or produced using computer software or simulation, i.e., virtual reality.

[0041] The terms “upstream” and “downstream” as used herein with respect to polynucleotides refer to “5' of” and “3' of”, respectively.

[0042] The term “expression” as used herein refers to (i) transcription of RNA (e.g., mRNA or a non-protein-coding RNA) from a coding region, and/or (ii) translation of a polypeptide from mRNA. Expression of a coding region of a polynucleotide sequence can be up-regulated or down-regulated in certain embodiments.

[0043] The term “operably linked” as used herein refers to the association of two or more nucleic acid sequences such that the function of one is affected by the other. For example, a promoter is operably linked with a coding sequence when it is capable of affecting the expression of that coding sequence. That is, the coding sequence is under the transcriptional control of the promoter. A coding sequence can be operably linked to one (e.g., promoter) or more (e.g., promoter and terminator) regulatory sequences, for example.

[0044] The term “recombinant” when used herein to characterize a DNA sequence such as a plasmid, vector, or construct refers to an artificial combination of two otherwise separated segments of sequence, e.g., by chemical synthesis

and/or by manipulation of isolated segments of nucleic acids by genetic engineering techniques.

[0045] The term “transformation” as used herein refers to the transfer of a nucleic acid molecule into a host organism or host cell by any method. A nucleic acid molecule that has been transformed into an organism/cell may be one that replicates autonomously in the organism/cell, or that integrates into the genome of the organism/cell, or that exists transiently in the cell without replicating or integrating. Non-limiting examples of nucleic acid molecules suitable for transformation are disclosed herein, such as plasmids and linear DNA molecules. Host organisms/cells herein containing a transforming nucleic acid sequence can be referred to as “transgenic”, “recombinant”, “transformed”, “engineered”, as a “transformant”, and/or as being “modified for exogenous gene expression”, for example.

[0046] The terms “sequence identity”, “identity” and the like as used herein with respect to polynucleotide or polypeptide sequences refer to the nucleic acid residues or amino acid residues in two sequences that are the same when aligned for maximum correspondence over a specified comparison window. Thus, “percentage of sequence identity”, “percent identity” and the like refer to the value determined by comparing two optimally aligned sequences over a comparison window, wherein the portion of the polynucleotide or polypeptide sequence in the comparison window may comprise additions or deletions (i.e., gaps) as compared to the reference sequence (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid base or amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the window of comparison and multiplying the results by 100 to yield the percentage of sequence identity. It would be understood that, when calculating sequence identity between a DNA sequence and an RNA sequence, T residues of the DNA sequence align with, and can be considered “identical” with, U residues of the RNA sequence. For purposes of determining “percent complementarity” of first and second polynucleotides, one can obtain this by determining (i) the percent identity between the first polynucleotide and the complement sequence of the second polynucleotide (or vice versa), for example, and/or (ii) the percentage of bases between the first and second polynucleotides that would create canonical Watson and Crick base pairs.

[0047] Percent identity can be readily determined by any known method, including but not limited to those described in: 1) *Computational Molecular Biology* (Lesk, A. M., Ed.) Oxford University: NY (1988); 2) *Biocomputing: Informatics and Genome Projects* (Smith, D. W., Ed.) Academic: NY (1993); 3) *Computer Analysis of Sequence Data, Part I* (Griffin, A. M., and Griffin, H. G., Eds.) Humana: NJ (1994); 4) *Sequence Analysis in Molecular Biology* (von Heinje, G., Ed.) Academic (1987); and 5) *Sequence Analysis Primer* (Gribbskov, M. and Devereux, J., Eds.) Stockton: NY (1991), all of which are incorporated herein by reference.

[0048] Preferred methods for determining percent identity are designed to give the best match between the sequences tested. Methods of determining identity and similarity are codified in publicly available computer programs, for example. Sequence alignments and percent identity calculations can be performed using the MEGALIGN program of

the LASERGENE bioinformatics computing suite (DNASTAR Inc., Madison, Wis.), for example. Multiple alignment of sequences can be performed, for example, using the Clustal method of alignment which encompasses several varieties of the algorithm including the Clustal V method of alignment (described by Higgins and Sharp, *CABIOS*. 5:151-153 (1989); Higgins, D. G. et al., *Comput. Appl. Biosci.*, 8:189-191 (1992)) and found in the MEGALIGN v8.0 program of the LASERGENE bioinformatics computing suite (DNASTAR Inc.). For multiple alignments, the default values can correspond to GAP PENALTY=10 and GAP LENGTH PENALTY=10. Default parameters for pairwise alignments and calculation of percent identity of protein sequences using the Clustal method can be KTUPLE=1, GAP PENALTY=3, WINDOW=5 and DIAGONALS SAVED=5. For nucleic acids, these parameters can be KTUPLE=2, GAP PENALTY=5, WINDOW=4 and DIAGONALS SAVED=4. Additionally, the Clustal W method of alignment can be used (described by Higgins and Sharp, *CABIOS*. 5:151-153 (1989); Higgins, D. G. et al., *Comput. Appl. Biosci.* 8:189-191(1992); Thompson, J. D. et al, 15 *Nucleic Acids Research*, 22 (22): 4673-4680, 1994) and found in the MEGALIGN v8.0 program of the LASERGENE bioinformatics computing suite (DNASTAR Inc.). Default parameters for multiple alignment (protein/nucleic acid) can be: GAP PENALTY=10/15, GAP LENGTH PENALTY=0.2/6.66, Delay Divergent Seqs (%)=30/30, DNA Transition Weight=0.5, Protein Weight Matrix=Gonnet Series, DNA Weight Matrix=IUB.

[0049] Various polypeptide amino acid sequences and polynucleotide sequences are disclosed herein as features of certain embodiments. Variants of these sequences that are at least about 70-85%, 85-90%, or 90%-95% identical to the sequences disclosed herein can be used or referenced. Alternatively, a variant amino acid sequence or polynucleotide sequence can have at least 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% identity with a sequence disclosed herein. The variant amino acid sequence or polynucleotide sequence has the same function/activity of the disclosed sequence, or at least about 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% of the function/activity of the disclosed sequence. Any polypeptide amino acid sequence disclosed herein not beginning with a methionine can typically further comprise at least a start-methionine at the N-terminus of the amino acid sequence. In contrast, any polypeptide amino acid sequence disclosed herein beginning with a methionine can optionally lack such a methionine residue.

[0050] The terms “aligns with”, “corresponds with”, and the like can be used interchangeably herein. Some embodiments herein relate to a glucosyltransferase comprising at least one amino acid substitution at a position corresponding with at least one particular amino acid residue of SEQ ID NO:62. An amino acid position of a glucosyltransferase or subsequence thereof (e.g., catalytic domain or catalytic domain plus glucan-binding domains) (can refer to such an amino acid position or sequence as a “query” position or sequence) can be characterized to correspond with a particular amino acid residue of SEQ ID NO:62 (can refer to such an amino acid position or sequence as a “subject” position or sequence) if (1) the query sequence can be

aligned with the subject sequence (e.g., where an alignment indicates that the query sequence and the subject sequence [or a subsequence of the subject sequence] are at least about 30%, 40%, 50%, 60%, 70%, 80%, or 90% identical), and (2) if the query amino acid position directly aligns with (directly lines up against) the subject amino acid position in the alignment of (1). In general, one can align a query amino acid sequence with a subject sequence (SEQ ID NO:62 or a subsequence of SEQ ID NO:62) using any alignment algorithm, tool and/or software described disclosed herein (e.g., BLASTP, ClustalW, ClustalV, Clustal-Omega, EMBOSS) to determine percent identity. Just for further example, one can align a query sequence with a subject sequence herein using the Needleman-Wunsch algorithm (Needleman and Wunsch, *J. Mol. Biol.* 48:443-453, 1970) as implemented in the Needle program of the European Molecular Biology Open Software Suite (EMBOSS [e.g., version 5.0.0 or later], Rice et al., *Trends Genet.* 16:276-277, 2000). The parameters of such an EMBOSS alignment can comprise, for example: gap open penalty of 10, gap extension penalty of 0.5, EBLOSUM62 (EMBOSS version of BLOSUM62) substitution matrix.

[0051] The numbering of particular amino acid residues of SEQ ID NO:62 herein (e.g., Asn-531, Arg-534, Thr-563, Glu-567, Val-586, Gln-588, Ile-591, Lys-593, Ile-608, Ala-610, Leu-661, Arg-722, Thr-728, Met-732, Arg-741, Asn-743, Ala-777, Tyr-848, Ile-1453) is with respect to the full-length amino acid sequence of SEQ ID NO:62. The first amino acid (i.e., position 1, Met-1) of SEQ ID NO:62 is at the start of the signal peptide. Unless otherwise disclosed, substitutions herein are with respect to the full-length amino acid sequence of SEQ ID NO:62.

[0052] A “non-native glucosyltransferase” herein (“mutant”, “variant”, “modified” and like terms can likewise be used to describe such a glucosyltransferase) has at least one amino acid substitution at a position corresponding with a particular amino acid residue of SEQ ID NO:62. Such at least one amino acid substitution typically is in place of the amino acid residue(s) that normally (natively) occurs at the same position in the native counterpart (parent) of the non-native glucosyltransferase (i.e., although SEQ ID NO:62 is used as a reference for position, an amino acid substitution herein is with respect to the native counterpart of a non-native glucosyltransferase) (considered another way, when aligning the sequence of a non-native glucosyltransferase with SEQ ID NO:62, determining whether a substitution exists at a particular position does not depend in-and-of-itself on the respective amino acid residue in SEQ ID NO:62, but rather depends on what amino acid exists at the subject position within the native counterpart of the non-native glucosyltransferase). The amino acid normally occurring at the relevant site in the native counterpart glucosyltransferase often (but not always) is the same as (or conserved with) the particular amino acid residue of SEQ ID NO:62 for which the alignment is made. A non-native glucosyltransferase optionally can have other amino acid changes (mutations, deletions, and/or insertions) relative to its native counterpart sequence.

[0053] It may be instructive to illustrate a substitution/alignment herein. SEQ ID NO:12 (GTF 0544) is a truncated form of a *Streptococcus sobrinus* glucosyltransferase. It is noted that Leu-193 of SEQ ID NO:12 corresponds with Leu-373 of SEQ ID NO:62 (alignment not shown). If SEQ ID NO:12 is mutated at position 193 to substitute the Leu

residue with a different residue (e.g., Gin), then it can be stated that the position 193-mutated version of SEQ ID NO:12 represents a non-native glucosyltransferase having an amino acid substitution at a position corresponding with Leu-373 of SEQ ID NO:62, for example.

[0054] The term “isolated” means a substance (or process) in a form or environment that does not occur in nature. Non-limiting examples of isolated substances include (1) any non-naturally occurring substance (e.g., a non-native glucosyltransferase herein), (2) any substance including, but not limited to, any host cell, enzyme, variant, nucleic acid, protein, peptide, cofactor, or carbohydrate/saccharide that is at least partially removed from one or more or all of the naturally occurring constituents with which it is associated in nature; (3) any substance modified by the hand of man relative to that substance found in nature (e.g., a non-native glucosyltransferase herein); or (4) any substance modified by increasing the amount of the substance relative to other components with which it is naturally associated. It is believed that the embodiments (e.g., enzymes and reaction compositions) disclosed herein are synthetic/man-made, and/or have properties that are not naturally occurring.

[0055] The term “increased” as used herein can refer to a quantity or activity that is at least about 1%, 2%, 3%, 4%, 5%, 6%, 7%, 8%, 9%, 10%, 11%, 12%, 13%, 14%, 15%, 16%, 17%, 18%, 19%, 20%, 50%, 100%, or 200% more than the quantity or activity for which the increased quantity or activity is being compared. The terms “increased”, “elevated”, “enhanced”, “greater than”, “improved” and the like are used interchangeably herein. These terms can be used to characterize the “over-expression” or “up-regulation” of a polynucleotide encoding a protein, for example.

[0056] While advances have been made in producing insoluble glucan polymers using glucosyltransferase enzymes, less attention appears to have been drawn to enhancing the molecular weight of insoluble glucan products synthesized by such enzymes. Addressing this technological gap, disclosed herein are glucosyltransferases with modified amino acid sequences that produce higher molecular weight insoluble glucan products.

[0057] Certain embodiments of the present disclosure concern a non-native glucosyltransferase comprising at least one amino acid substitution at a position corresponding with amino acid residue(s) Asn-531, Arg-534, Thr-563, Glu-567, Val-586, Gln-588, Ile-591, Lys-593, Ile-608, Ala-610, Leu-661, Arg-722, Thr-728, Met-732, Arg-741, Asn-743, Ala-777, Tyr-848, or Ile-1453 of SEQ ID NO:62, wherein the non-native glucosyltransferase synthesizes insoluble alpha-glucan comprising 1,3-linkages, and the molecular weight of this alpha-glucan is higher than the molecular weight of insoluble alpha-glucan synthesized by a second glucosyltransferase that only differs from the non-native glucosyltransferase at the substitution position(s). Thus, in general, mutant glucosyltransferase enzymes are disclosed herein that can synthesize higher molecular weight insoluble alpha-glucan having alpha-1,3 linkages.

[0058] A non-native glucosyltransferase herein synthesizes insoluble alpha-glucan comprising 1,3-linkages. In some aspects, at least about 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%,

85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, 99.5%, or 100% of the glycosidic linkages of such an alpha-glucan can be alpha-1,3 linkages. The linkage profile of an alpha-glucan can optionally be characterized as having a range between any two of these values. The other linkages in any of these aspects having 30%-99% alpha-1,3 linkages can be alpha-1,6, and/or not include any alpha-1,4 or alpha-1,2 linkages, for example.

[0059] Alpha-glucan in some aspects can have, for example, less than 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, 1%, or 0.5% of alpha-1,2 or alpha-1,4 glycosidic linkages. In another embodiment, an alpha-glucan only has alpha-1,3 and optionally alpha-1,6 linkages (i.e., no alpha-1,2 or alpha-1,4 linkages).

[0060] Alpha-glucan in some aspects can be linear/unbranched (no branch points). Alternatively, there can be branches in an alpha-glucan herein. For example, an alpha-glucan can have less than about 10%, 9%, 8%, 7%, 6%, 5%, 4%, 3%, 2%, or 1% branch points as a percent of the linkages in the polymer.

[0061] In certain aspects, an alpha-glucan can have a molecular weight in DP_w or DP_n of at least about 100. For example, the DP_w or DP_n can be about, or at least about, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, or 1200. The molecular weight of an alpha-glucan can optionally be expressed as a range between any two of these values (e.g., 100-1200, 400-1200, 700-1200, 100-1000, 400-1000, 700-1000). Molecular weight herein can be measured following any suitable method, including those methods disclosed in the present Examples (below) or as disclosed in U.S. Pat. Appl. Publ. Nos. 2017/0002335, 2015/0064748, or 2015/0232819, for example.

[0062] In certain aspects, the polydispersity index (PDI, which equals DP_w/DP_n) of alpha-1,3-glucan produced by a non-native glucosyltransferase can be the same as, or similar to, the PDI of alpha-1,3-glucan produced by a second glucosyltransferase (e.g., parent glucosyltransferase) that only differs from the non-native glucosyltransferase at the substitution position(s). The PDI can be at or below about 2.5, 2.4, 2.3, 2.2, 2.1, or 2.0, or range from about 2.0-2.5, 2.0-2.4, 2.0-2.3, 2.0-2.2, 2.1-2.5, 2.1-2.4, 2.1-2.3, or 2.1-2.2, for example. Amino acid substitutions providing a non-native glucosyltransferase herein can optionally be characterized to allow enzymatic synthesis of alpha-1,3-glucan with preserved PDI, but with increased molecular weight.

[0063] An alpha-glucan produced by a non-native glucosyltransferase herein is water-insoluble. Alpha-1,3-glucan is generally insoluble at a DP_w of 8 or 9 and above in neutral (e.g., pH 6-8) aqueous conditions.

[0064] Any of the foregoing linkage profiles and/or molecular weight profiles, for example, can be combined herein to appropriately characterize an alpha-glucan product of a non-native glucosyltransferase of the present disclosure. In some aspects, the linkage and/or molecular weight profile of an alpha-glucan product can be as disclosed in any of the following publications, all of which are incorporated herein by reference: U.S. Pat. Nos. 7,000,000 and 8,871,474, U.S. Patent Appl. Publ. No. 2015/0232819.

[0065] A non-native glucosyltransferase, for example, can comprise the amino acid sequence of any glucosyltransferase disclosed in the following publications that is capable of producing insoluble alpha-glucan as presently disclosed,

but with the exception that the non-native glucosyltransferase comprises at least one amino acid substitution at a position corresponding with amino acid residue Asn-531, Arg-534, Thr-563, Glu-567, Val-586, Gln-588, Ile-591, Lys-593, Ile-608, Ala-610, Leu-661, Arg-722, Thr-728, Met-732, Arg-741, Asn-743, Ala-777, Tyr-848, or Ile-1453 of SEQ ID NO:62: U.S. Pat. Nos. 7,000,000 and 8,871,474; and U.S. Patent Appl. Publ. Nos. 2015/0232819 and 2017/0002335, all of which are incorporated herein by reference. In some aspects, such a non-native glucosyltransferase (i) has at least one of the foregoing substitutions, and (ii) comprises an amino acid sequence that is at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 99.5% identical to the amino acid sequence of the respective counterpart/parent glucosyltransferase not having the at least one substitution.

[0066] In some aspects, a non-native glucosyltransferase (i) comprises at least one amino acid substitution at a position corresponding with amino acid residue Asn-531, Arg-534, Thr-563, Glu-567, Val-586, Gln-588, Ile-591, Lys-593, Ile-608, Ala-610, Leu-661, Arg-722, Thr-728, Met-732, Arg-741, Asn-743, Ala-777, Tyr-848, or Ile-1453 of SEQ ID NO:62, and (ii) comprises or consists of an amino acid sequence that is at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 99.5% identical to SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 26, 28, 30, 34, or 59. Certain information regarding insoluble alpha-glucan products of glucosyltransferases with most of these amino acid sequences is provided in Table 2.

TABLE 2

GTF Enzymes and Related Alpha-Glucan Products ^a						
GTF ID	SEQ ID NO.	Reducing Sugars	Insoluble Product	Linkages		DP _n
				% alpha-1,3	% alpha-1,6	
0874	2	yes	yes	100	0	60
6855	4	yes	yes	100	0	440
2379	6	yes	yes	37	63	310
7527	8	yes	yes	100	0	440
1724	10	yes	yes	100	0	250
0544	12	yes	yes	62	36	980
5926	14	yes	yes	100	0	260
4297	16	yes	yes	31	67	800
5618	18	yes	yes	34	66	1020
2765	20	yes	yes	100	0	280
0427	26	yes	yes	100	0	120
2919	28	yes	yes	100	0	250
2678	30	yes	yes	100	0	390
3929	34	yes	yes	100	0	280

^aGTF reactions and product analyses were performed as follows. Reactions were prepared comprising sucrose (50 g/L), potassium phosphate buffer (pH 6.5; 20 mM) and a GTF enzyme (2.5% bacterial cell extract by volume; extracts prepared according to U.S. application Pub. No. 2017/0002335, in a manner similar to procedure disclosed in U.S. Pat. No. 8,871,474). After 24-30 hours at 22-25° C., insoluble product was harvested by centrifugation, washed three times with water, washed once with ethanol, and dried at 50° C. for 24-30 hours. Approximate linkages and DP_n are shown for each insoluble product. Linkages and DP_n were determined by ¹³C NMR and SEC, respectively.

[0067] In some aspects, a non-native glucosyltransferase (i) comprises at least one amino acid substitution at a position corresponding with amino acid residue Asn-531, Arg-534, Thr-563, Glu-567, Val-586, Gln-588, Ile-591, Lys-593, Ile-608, Ala-610, Leu-661, Arg-722, Thr-728, Met-732, Arg-741, Asn-743, Ala-777, Tyr-848, or Ile-1453 of SEQ ID NO:62, and (ii) comprises or consists of a glucosyltransferase catalytic domain that is at least about 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 99.5% identical

to amino acid residues 55-960 of SEQ ID NO:4, residues 54-957 of SEQ ID NO:65, residues 55-960 of SEQ ID NO:30, residues 55-960 of SEQ ID NO:28, or residues 55-960 of SEQ ID NO:20. Such a non-native glucosyltransferase, for instance, is believed to be able to produce alpha-glucan that is water-insoluble and comprise at least about 50% (e.g., ≥90% or ≥95%) alpha-1,3 linkages, and optionally further have a DP_w of at least 100. It is noted that a glucosyltransferase with amino acid positions 54-957 of SEQ ID NO:65 can produce alpha-1,3-glucan with 100% alpha-1,3 linkages and a DP_w of at least 400 (data not shown, refer to Table 6 of U.S. Pat. Appl. Publ. No. 2017/0002335, which is incorporated herein by reference), for example. It is further noted that SEQ ID NOs:65 (GTF 7527), 30 (GTF 2678), 4 (GTF 6855), 28 (GTF 2919), and 20 (GTF 2765) each represent a glucosyltransferase that, compared to its respective wild type counterpart, lacks the signal peptide domain and all or a substantial portion of the variable domain. Thus, each of these glucosyltransferase enzymes has a catalytic domain followed by a glucan-binding domain. The approximate location of catalytic domain sequences in these enzymes is as follows: 7527 (residues 54-957 of SEQ ID NO:65), 2678 (residues 55-960 of SEQ ID NO:30), 6855 (residues 55-960 of SEQ ID NO:4), 2919 (residues 55-960 of SEQ ID NO:28), 2765 (residues 55-960 of SEQ ID NO:20). The amino acid sequences of the catalytic domains (approx.) of GTFs 2678, 6855, 2919 and 2765 have about 94.9%, 99.0%, 95.5% and 96.4% identity, respectively, with the approximate catalytic domain sequence of GTF 7527 (i.e., amino acids 54-957 of SEQ ID NO:65). Each of these particular glucosyltransferases (GTFs 2678, 6855, 2919 and 2765) can produce alpha-1,3-glucan with 100% alpha-1,3 linkages and a DP_w of at least 400 (data not shown, refer to Table 4 of U.S. Pat. Appl. Publ. No. 2017/0002335). Based on this activity, and the relatedness (high percent identity) of the foregoing catalytic domains, it is contemplated that a non-native glucosyltransferase herein having one of the foregoing catalytic domains further with at least one amino acid substitution as presently disclosed can produce insoluble alpha-glucan comprising at least about 50% (e.g., ≥90% or ≥95%) alpha-1,3 linkages and a DP_w of at least 100.

[0068] In some aspects, a non-native glucosyltransferase (i) comprises at least one amino acid substitution at a position corresponding with amino acid residue Asn-531, Arg-534, Thr-563, Glu-567, Val-586, Gln-588, Ile-591, Lys-593, Ile-608, Ala-610, Leu-661, Arg-722, Thr-728, Met-732, Arg-741, Asn-743, Ala-777, Tyr-848, or Ile-1453 of SEQ ID NO:62, and (ii) comprises or consists of an amino acid sequence that is at least about 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 99.5% identical to SEQ ID NO:62 or a subsequence thereof such as SEQ ID NO:4 (without start methionine thereof) or positions 55-960 of SEQ ID NO:4 (approximate catalytic domain).

[0069] Although it is believed that a non-native glucosyltransferase in certain aspects need only have a catalytic domain, the non-native glucosyltransferase can be comprised within a larger amino acid sequence. For example, a catalytic domain may be linked at its C-terminus to a

glucan-binding domain, and/or linked at its N-terminus to a variable domain and/or signal peptide.

[0070] Although amino acid substitutions in a non-native glucosyltransferase are generally disclosed herein with respect to the corresponding positions in SEQ ID NO:62, such substitutions can alternatively be stated simply with respect to its position number in the sequence of the non-native glucosyltransferase itself, as convenience may dictate.

[0071] Still further examples of non-native glucosyltransferases can be any as disclosed herein and that include 1-300 (or any integer there between [e.g., 10, 15, 20, 25, 30, 35, 40, 45, or 50]) residues on the N-terminus and/or C-terminus. Such additional residues may be from a corresponding wild type sequence from which the glucosyltransferase enzyme is derived, or may be a heterologous sequence such as an epitope tag (at either N- or C-terminus) or a heterologous signal peptide (at N-terminus), for example. A non-native glucosyltransferase herein typically lacks an N-terminal signal peptide; such an enzyme can optionally be characterized as being mature if its signal peptide was removed during a secretion process.

[0072] A non-native glucosyltransferase herein can be derived from any microbial source, for example, such as bacteria. Examples of bacterial glucosyltransferases are those derived from a *Streptococcus* species, *Leuconostoc* species, or *Lactobacillus* species. Examples of *Streptococcus* species include *S. salivarius*, *S. sobrinus*, *S. dentirosetti*, *S. downei*, *S. mutans*, *S. oralis*, *S. gallolyticus* and *S. sanguinis*. Examples of *Leuconostoc* species include *L. mesenteroides*, *L. amelibiosum*, *L. argentinum*, *L. carnosum*, *L. citreum*, *L. cremoris*, *L. dextranicum* and *L. fructosum*. Examples of *Lactobacillus* species include *L. acidophilus*, *L. delbrueckii*, *L. helveticus*, *L. salivarius*, *L. casei*, *L. curvatus*, *L. plantarum*, *L. sakei*, *L. brevis*, *L. buchneri*, *L. fermentum* and *L. reuteri*.

[0073] A non-native glucosyltransferase herein can be prepared by fermentation of an appropriately engineered microbial strain, for example. Recombinant enzyme production by fermentation is well known in the art using microbial species such as *E. coli*, *Bacillus* strains (e.g., *B. subtilis*), *Ralstonia eutropha*, *Pseudomonas fluorescens*, *Saccharomyces cerevisiae*, *Pichia pastoris*, *Hansenula polymorpha*, and species of *Aspergillus* (e.g., *A. awamori*) and *Trichoderma* (e.g., *T. reesei*) (e.g., see Adrio and Demain, *Biomolecules* 4:117-139, 2014, which is incorporated herein by reference). A nucleotide sequence encoding a non-native glucosyltransferase amino acid sequence is typically linked to a heterologous promoter sequence to create an expression cassette for the enzyme, and/or is codon-optimized accordingly. Such an expression cassette may be incorporated in a suitable plasmid or integrated into the microbial host chromosome, using methods well known in the art. The expression cassette may include a transcriptional terminator nucleotide sequence following the amino acid coding sequence. The expression cassette may also include, between the promoter sequence and glucosyltransferase amino acid coding sequence, a nucleotide sequence encoding a signal peptide (e.g., heterologous signal peptide) that is designed for direct secretion of the glucosyltransferase enzyme. At the end of fermentation, cells may be ruptured accordingly (generally when a signal peptide for secretion is not employed) and the glucosyltransferase enzyme can be isolated using methods such as precipitation, filtration, and/

or concentration. Alternatively, a lysate or extract comprising a glucosyltransferase can be used without further isolation. If the glucosyltransferase was secreted (i.e., it is present in the fermentation broth), it can optionally be used as isolated from, or as comprised in, the fermentation broth. The activity of a glucosyltransferase enzyme can be confirmed by biochemical assay, such as measuring its conversion of sucrose to glucan polymer.

[0074] A non-native glucosyltransferase herein can comprise at least one amino acid substitution at a position corresponding with amino acid residue Asn-531, Arg-534, Thr-563, Glu-567, Val-586, Gln-588, Ile-591, Lys-593, Ile-608, Ala-610, Leu-661, Arg-722, Thr-728, Met-732, Arg-741, Asn-743, Ala-777, Tyr-848, or Ile-1453 of SEQ ID NO:62. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Asn-531 of SEQ ID NO:62 can be with a Gly, Leu, or Met residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Arg-534 of SEQ ID NO:62 can be with a Lys, Gly, Ile, Leu, or Met residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Thr-563 of SEQ ID NO:62 can be with an Ala residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Glu-567 of SEQ ID NO:62 can be with a Gln residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Val-586 of SEQ ID NO:62 can be with a Thr residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Gln-588 of SEQ ID NO:62 can be with a Leu residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Ile-591 of SEQ ID NO:62 can be with a Val, Lys, or Arg residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Lys-593 of SEQ ID NO:62 can be with a Met residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Ile-608 of SEQ ID NO:62 can be with a Tyr residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Ala-610 of SEQ ID NO:62 can be with a Cys or Thr residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Leu-661 of SEQ ID NO:62 can be with a Pro residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Arg-722 of SEQ ID NO:62 can be with a His or Asn residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Thr-728 of SEQ ID NO:62 can be with a Ser residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Met-732 of SEQ ID NO:62 can be with a Leu residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Arg-741 of SEQ ID NO:62 can be with a Ser, Ala, Pro, Gln, or Thr residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Asn-743 of SEQ ID NO:62 can be with a Ser, Thr, or Asp residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Ala-777 of SEQ ID NO:62 can be with an Asn residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Tyr-848 of SEQ ID NO:62 can be with a Glu residue. In some aspects, the amino acid substitution

at a position corresponding with amino acid residue Ile-1453 of SEQ ID NO:62 can be with a Gly or Met residue.

[0075] A non-native glucosyltransferase in certain embodiments can comprise, in addition to any of the above-listed substitution(s), or alternatively to the above-listed substitution(s), at least one amino acid substitution at a position corresponding with amino acid residue Phe-424, Asn-475, Trp-511, Arg-609, Asn-614, or Asn-1214 of SEQ ID NO:62. Such a non-native glucosyltransferase can be based on any of the above-disclosed glucosyltransferase/catalytic domain amino acid sequences (and percent identities thereto), for example. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Phe-424 of SEQ ID NO:62 can be with an Ala, Val, Leu, Glu, or Gln residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Asn-475 of SEQ ID NO:62 can be with a Gln or Ser residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Trp-511 of SEQ ID NO:62 can be with a Tyr residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Arg-609 of SEQ ID NO:62 can be with a His residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Asn-614 of SEQ ID NO:62 can be with a Phe residue. In some aspects, the amino acid substitution at a position corresponding with amino acid residue Asn-1214 of SEQ ID NO:62 can be with a Leu or Ile residue.

[0076] A non-native glucosyltransferase herein can comprise one, two, three, four, five, six, seven, eight, nine, or more of the presently disclosed amino acid substitutions, for instance. A non-native glucosyltransferase in some aspects can comprise at least one amino acid substitution at a position corresponding with amino acid residue Gln-588, Arg-741, or Arg-722 of SEQ ID NO:62. In some aspects, a non-native glucosyltransferase can comprise substitutions at one of these sites (e.g., Q588), two of these sites (e.g., Q588 and R741), or all three of these sites (Q588, R741 and Arg-722). Such an amino acid substitution(s) can be any of those as disclosed above, for example (e.g., Q588L, R741S, R722H). In some aspects, a non-native glucosyltransferase can comprise substitutions at one, two or all three of these sites, and have a total number of the presently disclosed substitutions as disclosed above.

[0077] Suitable substitution sites, and examples of particular substitutions at these sites, can include those as listed in Table 3 in Example 1 (below) that are associated with an increase in the molecular weight (DP_w) of alpha-1,3-glucan product by at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, or 60%, for example. In some alternative aspects, a substitution site, and example(s) of particular substitution(s) at such site, can include any of those as listed in Table 3 in Example 1 (below) that are associated with a feature that endows a benefit to a glucosyltransferase that synthesizes insoluble alpha-1,3-glucan. The foregoing substitutions as listed in Table 3 are as they correspond with the listed residue position number in SEQ ID NO:62. In some aspects, one or more substitutions are conserved or non-conserved substitutions; such conservation (or not) can be, for instance, with respect to the amino acid that occurs in the native glucosyltransferase from which the non-native glucosyltransferase is derived.

[0078] A non-native glucosyltransferase herein can synthesize insoluble alpha-glucan comprising 1,3-linkages with

a molecular weight higher than the molecular weight of insoluble alpha-glucan comprising 1,3-linkages synthesized by a second glucosyltransferase (or, simply, "another" glucosyltransferase) (e.g., parent glucosyltransferase) that only differs from the non-native glucosyltransferase at the substitution position(s). A second glucosyltransferase herein, for example, can be comprised of all of, or mostly, native amino acid sequence. Thus, while a second glucosyltransferase herein can be a native glucosyltransferase in some aspects, it can be a prior-modified glucosyltransferase in other aspects (e.g., a glucosyltransferase with one or more other amino acid substitutions differing from the substitution [s] of the present disclosure). In some embodiments, a second glucosyltransferase to which a non-native glucosyltransferase is compared has a native amino acid residue(s) at the substitution position(s). Determining whether an amino acid residue is native can be done by comparing the second glucosyltransferase amino acid sequence to the native/wild type glucosyltransferase amino acid sequence from which the second glucosyltransferase is derived.

[0079] In some aspects, a non-native glucosyltransferase herein can synthesize insoluble alpha-glucan with a molecular weight that is at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, or 60% higher than the molecular weight of insoluble alpha-glucan synthesized by a second glucosyltransferase. Such a determination can be made with respect to any glucan synthesis reaction/process as disclosed herein (e.g., taking into account initial sucrose conc., temperature, pH, and/or reaction time), and using any suitable measurement technique (e.g., SEC). Typically, a comparison between non-native and second glucosyltransferases herein can be made under identical or similar reaction conditions. The molecular weight of insoluble alpha-glucan can be expressed as DP_w , for example.

[0080] Some embodiments disclosed herein concern a polynucleotide comprising a nucleotide sequence that encodes a non-native glucosyltransferase as presently disclosed (e.g., a non-native glucosyltransferase comprising at least one amino acid substitution at a position corresponding with amino acid residue Asn-531, Arg-534, Thr-563, Glu-567, Val-586, Gln-588, Ile-591, Lys-593, Ile-608, Ala-610, Leu-661, Arg-722, Thr-728, Met-732, Arg-741, Asn-743, Ala-777, Tyr-848, or Ile-1453 of SEQ ID NO:62). Optionally, one or more regulatory sequences are operably linked to the nucleotide sequence, and preferably a promoter sequence is included as a regulatory sequence.

[0081] A polynucleotide comprising a nucleotide sequence encoding a non-native glucosyltransferase herein can be a vector or construct useful for transferring a nucleotide sequence into a cell, for example. Examples of a suitable vector/construct can be selected from a plasmid, yeast artificial chromosome (YAC), cosmid, phagemid, bacterial artificial chromosome (BAC), virus, or linear DNA (e.g., linear PCR product). A polynucleotide sequence in some aspects can be capable of existing transiently (i.e., not integrated into the genome) or stably (i.e., integrated into the genome) in a cell. A polynucleotide sequence in some aspects can comprise, or lack, one or more suitable marker sequences (e.g., selection or phenotype marker).

[0082] A polynucleotide sequence in certain embodiments can comprise one or more regulatory sequences operably linked to the nucleotide sequence encoding a non-native glucosyltransferase. For example, a nucleotide sequence encoding a non-native glucosyltransferase may be in oper-

able linkage with a promoter sequence (e.g., a heterologous promoter). A promoter sequence can be suitable for expression in a cell (e.g., bacterial cell such as *E. coli* or *Bacillus*; eukaryotic cell such as a fungus, yeast, insect, or mammalian cell) or in an in vitro protein expression system, for example. Examples of other suitable regulatory sequences include transcription terminator sequences.

[0083] Some aspects herein are drawn to a cell comprising a polynucleotide sequence as presently disclosed; such a cell can be any type disclosed herein (e.g., bacterial cell such as *E. coli* or *Bacillus*; eukaryotic cell such as a fungus, yeast, insect, or mammalian cell). A cell can optionally express a non-native glucosyltransferase encoded by the polynucleotide sequence. In some aspects, the polynucleotide sequence exists transiently (i.e., not integrated into the genome) or stably (i.e., integrated into the genome) in the cell.

[0084] Some embodiments disclosed herein concern reaction compositions comprising water, sucrose, and one or more non-native glucosyltransferases herein (e.g., a non-native glucosyltransferase comprising at least one amino acid substitution at a position corresponding with amino acid residue Asn-531, Arg-534, Thr-563, Glu-567, Val-586, Gln-588, Ile-591, Lys-593, Ile-608, Ala-610, Leu-661, Arg-722, Thr-728, Met-732, Arg-741, Asn-743, Ala-777, Tyr-848, or Ile-1453 of SEQ ID NO:62). Such a reaction composition produces, at least, alpha-glucan comprising 1,3-linkages as disclosed.

[0085] The temperature of a reaction composition herein can be controlled, if desired, and can be about 5-50° C., 20-40° C., 30-40° C., 20-30° C., 20-25° C., 20° C., 25° C., 30° C., 35° C., or 40° C., for example.

[0086] The initial concentration of sucrose in a reaction composition herein can be about 20-400 g/L, 75-175 g/L, or 50-150 g/L, for example. In some aspects, the initial sucrose concentration is at least about 50, 75, 100, 150 or 200 g/L, or is about 50-600 g/L, 100-500 g/L, 50-100 g/L, 100-200 g/L, 150-450 g/L, 200-450 g/L, or 250-600 g/L. "Initial concentration of sucrose" refers to the sucrose concentration in a reaction composition just after all the reaction components have been added/combined (e.g., at least water, sucrose, non-native glucosyltransferase enzyme).

[0087] The pH of a reaction composition in certain embodiments can be about 4.0-9.0, 4.0-8.5, 4.0-8.0, 5.0-8.0, 5.5-7.5, or 5.5-6.5. In some aspects, the pH can be about 4.0, 4.5, 5.0, 5.5, 6.0, 6.5, 7.0, 7.5, or 8.0. The pH can be adjusted or controlled by the addition or incorporation of a suitable buffer, including but not limited to: phosphate, tris, citrate, or a combination thereof. The buffer concentration in a reaction composition herein can be about 0.1-300 mM, 0.1-100 mM, 10-100 mM, 10 mM, 20 mM, or 50 mM, for example.

[0088] A reaction composition can be contained within any vessel (e.g., an inert vessel/container) suitable for applying one or more of the reaction conditions disclosed herein. An inert vessel in some aspects can be of stainless steel, plastic, or glass (or comprise two or more of these components) and be of a size suitable to contain a particular reaction. For example, the volume/capacity of an inert vessel (and/or the volume of a reaction composition herein), can be about, or at least about, 1, 10, 50, 100, 500, 1000, 2500, 5000, 10000, 12500, 15000, or 20000 liters. An inert vessel can optionally be equipped with a stirring device.

[0089] A reaction composition herein can contain one, two, or more glucosyltransferase enzymes, for example, just as long that at least one of the enzymes is a non-native glucosyltransferase as presently disclosed. In some embodiments, only one or two glucosyltransferase enzymes is/are comprised in a reaction composition. A glucosyltransferase reaction herein can be, and typically is, cell-free (e.g., no whole cells present).

[0090] Any of the features disclosed herein (e.g., above and in the below Examples) regarding a reaction composition can characterize appropriate aspects of a glucan production method herein, and vice versa.

[0091] The present disclosure also concerns a method for producing insoluble alpha-glucan, the method comprising: (a) contacting at least water, sucrose, and at least one non-native glucosyltransferase as disclosed herein that produces insoluble alpha-glucan, whereby insoluble alpha-glucan is produced; and b) optionally, isolating the insoluble alpha-glucan produced in step (a). Conducting such a method, which can optionally be characterized as a glucan synthesis method, is typically also performed when conducting a reaction composition herein.

[0092] A glucan synthesis method as presently disclosed comprises contacting at least water, sucrose, and a non-native glucosyltransferase herein that produces insoluble alpha-glucan. These and optionally other reagents can be added altogether or in any order as discussed below. This step can optionally be characterized as providing a reaction composition comprising water, sucrose and a non-native glucosyltransferase enzyme that synthesizes insoluble alpha-glucan. The contacting step herein can be performed in any number of ways. For example, the desired amount of sucrose can first be dissolved in water (optionally, other components may also be added at this stage of preparation, such as buffer components), followed by addition of glucosyltransferase enzyme. The solution may be kept still, or agitated via stirring or orbital shaking, for example. A glucan synthesis method can be performed by batch, fed-batch, continuous mode, or by any variation of these modes.

[0093] Completion of a reaction in certain embodiments can be determined visually (e.g., no more accumulation of insoluble glucan), and/or by measuring the amount of sucrose left in the solution (residual sucrose), where a percent sucrose consumption of at least about 90%, 95%, or 99% can indicate reaction completion. A reaction of the disclosed process can be conducted for about 1 hour to about 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 36, 48, 60, 72, 96, 120, 144, or 168 hours, for example.

[0094] The molecular weight of insoluble alpha-glucan produced in some aspects of a glucan synthesis method herein can be at least about 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, or 60% higher than the molecular weight of insoluble alpha-glucan synthesized by a second glucosyltransferase. Such molecular weight enhancement in some aspects is achieved in a reaction conducted for about 16-24 hours (e.g., ~20 hours).

[0095] Insoluble alpha-glucan produced in a method herein can optionally be isolated. In certain embodiments, isolating insoluble alpha-glucan can include at least conducting a step of centrifugation and/or filtration. Isolation can optionally further comprise washing alpha-glucan one, two, or more times with water or other aqueous liquid, and/or drying the alpha-glucan product.

[0096] An isolated alpha-glucan product herein, as provided in a dry form, can comprise no more than 2.0, 1.5, 1.0, 0.5, 0.25, 0.10, 0.05, or 0.01 wt % water, for example. In some aspects, an alpha-glucan product is provided in an amount of at least 1 gram (e.g., at least about 2.5, 5, 10, 25, 50, 100, 250, 500, 750, 1000, 2500, 5000, 7500, 10000, 25000, 50000, or 100000 g); such an amount can be a dry amount, for example.

[0097] Any of the disclosed conditions for synthesizing an alpha-glucan, such as the foregoing or those described in the below Examples, can be applied to practicing a reaction composition as presently disclosed (and vice versa), and/or used to characterize features/activity of a non-native glucosyltransferase, accordingly.

[0098] The present disclosure also concerns a method of preparing a polynucleotide sequence encoding a non-native glucosyltransferase herein. This method comprises:

[0099] (a) identifying a polynucleotide sequence encoding a parent glucosyltransferase that (i) comprises an amino acid sequence that is at least about 40% identical to SEQ ID NO:4 or positions 55-960 of SEQ ID NO:4, and (ii) synthesizes insoluble alpha-glucan comprising 1,3-linkages; and

[0100] (b) modifying the polynucleotide sequence identified in step (a) to substitute at least one amino acid of the parent glucosyltransferase at a position corresponding with amino acid residue Asn-531, Arg-534, Thr-563, Glu-567, Val-586, Gln-588, Ile-591, Lys-593, Ile-608, Ala-610, Leu-661, Arg-722, Thr-728, Met-732, Arg-741, Asn-743, Ala-777, Tyr-848, or Ile-1453 of SEQ ID NO:62, thereby providing a polynucleotide sequence encoding a non-native glucosyltransferase that synthesizes insoluble alpha-glucan with a molecular weight that is higher than the molecular weight of insoluble alpha-glucan synthesized by the parent glucosyltransferase.

Such a method can optionally further comprise using a polynucleotide prepared in this manner in a method of expressing the non-native glucosyltransferase encoded by the polynucleotide. Such an expression method can follow any heterologous protein expression method as known in the art, for example. The present method of preparing a polynucleotide can optionally alternatively be characterized as a method of increasing the product molecular weight of a glucosyltransferase.

[0101] Identification step (a) herein can, in some instances, comprise identifying an amino acid sequence of a parent glucosyltransferase enzyme. A polynucleotide sequence could be determined from this amino acid sequence according to the genetic code (codons), such as the genetic code used in the species from which the parent glucosyltransferase was identified.

[0102] Identifying a polynucleotide encoding a parent glucosyltransferase herein can be performed (a) in silico, (b) with a method comprising a nucleic acid hybridization step, (c) with a method comprising a protein sequencing step, and/or (d) with a method comprising a protein binding step, for example.

[0103] Regarding in silico detection, the amino acid sequences of candidate parent glucosyltransferase enzymes (and/or nucleotide sequences encoding such glucosyltransferase enzymes) stored in a computer or database (e.g., public databases such as GENBANK, EMBL, REFSEQ, GENEPEPT, SWISS-PROT, PIR, PDB) can be reviewed in silico to identify a glucosyltransferase enzyme comprising

an amino acid sequence with a percent sequence identity as described above for a parent glucosyltransferase. Such review could comprise using any means known in the art such as through use of an alignment algorithm or software as described above (e.g., BLASTN, BLASTP, ClustalW, ClustalV, Clustal-Omega, EMBOSS).

[0104] Identifying a parent glucosyltransferase as disclosed above can optionally be performed via a method comprising a nucleic acid hybridization step. Such a method can comprise using DNA hybridization (e.g., Southern blot, dot blot), RNA hybridization (e.g., northern blot), or any other method that has a nucleic acid hybridization step (e.g., DNA sequencing, PCR, RT-PCR, all of which may comprise hybridization of an oligonucleotide), for example. A polynucleotide sequence encoding SEQ ID NO:4 or a subsequence thereof (e.g., positions 55-960 of SEQ ID NO:4) can be used as a probe, for example, in such a hybridization. Conditions and parameters for carrying out hybridization methods in general are well known and disclosed, for example, in Sambrook J, Fritsch E F and Maniatis T, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory: Cold Spring Harbor, N.Y. (1989); Silhavy T J, Bennis M L and Enquist L W, *Experiments with Gene Fusions*, Cold Spring Harbor Laboratory: Cold Spring Harbor, N.Y. (1984); Ausubel F M et al., *Current Protocols in Molecular Biology*, published by Greene Publishing Assoc. and Wiley-Interscience, Hoboken, N.J. (1987); and Innis M A, Gelfand D H, Sninsky J J and White T J (Editors), *PCR Protocols: A Guide to Methods and Applications*, Academic Press, Inc., San Diego, Calif. (1990).

[0105] Identifying a parent glucosyltransferase as disclosed above can optionally be performed via a method comprising a protein sequencing step. Such a protein sequencing step can comprise one or more procedures such as N-terminal amino acid analysis, C-terminal amino acid analysis, Edman degradation, or mass spectrometry, for example.

[0106] Identifying a parent glucosyltransferase as disclosed above can optionally be performed via a method comprising a protein binding step. Such a protein binding step can be performed using an antibody that binds to a motif or epitope within SEQ ID NO:4 (e.g., within positions 55-960 of SEQ ID NO:4), for example.

[0107] A polynucleotide identified in step (a) (i.e., before its modification in step [b]) can, in some aspects, encode a glucosyltransferase comprising an amino acid sequence that is identical to, or at least 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to, the amino acid sequence of any glucosyltransferase disclosed in Table 1. An alpha-glucan as produced by such a glucosyltransferase can be as disclosed herein, for example.

[0108] A method of preparing a polynucleotide sequence encoding a non-native glucosyltransferase herein comprises step (b) of modifying the polynucleotide sequence (encoding a parent glucosyltransferase) identified in step (a). Such modification substitutes at least one amino acid of the parent glucosyltransferase at a position corresponding with amino acid residue Asn-531, Arg-534, Thr-563, Glu-567, Val-586, Gln-588, Ile-591, Lys-593, Ile-608, Ala-610, Leu-661, Arg-722, Thr-728, Met-732, Arg-741, Asn-743, Ala-777, Tyr-848, or Ile-1453 of SEQ ID NO:62. The non-native glucosyltransferase (encoded by the modified polynucleotide

sequence) resulting from such one or more substitutions can be optionally be characterized as a “child glucosyltransferase” herein.

[0109] A parent glucosyltransferase enzyme herein can comprise an amino acid sequence that is at least about 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 69%, 70%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99%, or 99.5% identical to SEQ ID NO:4 (optionally without start methionine thereof) or positions 55-960 of SEQ ID NO:4 (approximate catalytic domain), for example. It is noted simply for reference purposes that SEQ ID NO:4 without its start methionine is a subsequence of SEQ ID NO:62.

[0110] A suitable modification of a polynucleotide in step (b) can be made following any DNA manipulation technique known in the art. Modifying step (b) can optionally be performed in silico, followed by synthesis of the polynucleotide sequence encoding a non-native glucosyltransferase. For example, a polynucleotide sequence identified in step (a) can be manipulated in silico using a suitable sequence manipulation program/software (e.g., VECTOR NTI, Life Technologies, Carlsbad, Calif.; DNASTrider; DNASTAR, Madison, Wis.). Following such virtual manipulation, the modified polynucleotide sequence can be artificially synthesized by any suitable technique (e.g., annealing-based connection of oligonucleotides, or any technique disclosed in Hughes et al., *Methods Enzymol.* 498:277-309, which is incorporated herein by reference). It should be appreciated that the foregoing methodology is not believed to necessarily rely on having a pre-existing polynucleotide (encoding a parent glucosyltransferase) in hand.

[0111] Modifying step (b) can optionally be performed using a physical copy of a polynucleotide sequence identified in step (a) encoding a parent glucosyltransferase. As an example, such a polynucleotide can serve as a template for amplification using primers designed in a manner such that the amplified product encodes a non-native glucosyltransferase herein (e.g., refer to Innis et al., *ibid.*).

[0112] The amino acid substitutions in this method can be any of those combinations of substitutions as disclosed herein. Essentially any non-native glucosyltransferase as presently disclosed can be encoded by a polynucleotide as prepared by this method, for instance.

[0113] Non-limiting examples of compositions and methods disclosed herein include:

1. A non-native glucosyltransferase comprising at least one amino acid substitution at a position corresponding with amino acid residue Asn-531, Arg-534, Thr-563, Glu-567, Val-586, Gln-588, Ile-591, Lys-593, Ile-608, Ala-610, Leu-661, Arg-722, Thr-728, Met-732, Arg-741, Asn-743, Ala-777, Tyr-848, or Ile-1453 of SEQ ID NO:62, wherein the non-native glucosyltransferase synthesizes insoluble alpha-glucan comprising 1,3-linkages, and the molecular weight of the insoluble alpha-glucan is higher than the molecular weight of insoluble alpha-glucan synthesized by a second glucosyltransferase that only differs from the non-native glucosyltransferase at the substitution position(s).
2. The non-native glucosyltransferase of embodiment 1, wherein: (i) the amino acid substitution at the position corresponding with amino acid residue Asn-531 is with a Gly, Leu, or Met residue; (ii) the amino acid substitution at

the position corresponding with amino acid residue Arg-534 is with a Lys, Gly, Ile, Leu, or Met residue; (iii) the amino acid substitution at the position corresponding with amino acid residue Thr-563 is with an Ala residue; (iv) the amino acid substitution at the position corresponding with amino acid residue Glu-567 is with a Gin residue; (v) the amino acid substitution at the position corresponding with amino acid residue Val-586 is with a Thr residue; (vi) the amino acid substitution at the position corresponding with amino acid residue Gln-588 is with a Leu residue; (vii) the amino acid substitution at the position corresponding with amino acid residue Ile-591 is with a Val, Lys, or Arg residue; (viii) the amino acid substitution at the position corresponding with amino acid residue Lys-593 is with a Met residue; (ix) the amino acid substitution at the position corresponding with amino acid residue Ile-608 is with a Tyr residue; (x) the amino acid substitution at the position corresponding with amino acid residue Ala-610 is with a Cys or Thr residue; (xi) the amino acid substitution at the position corresponding with amino acid residue Leu-661 is with a Pro residue; (xii) the amino acid substitution at the position corresponding with amino acid residue Arg-722 is with a His or Asn residue; (xiii) the amino acid substitution at the position corresponding with amino acid residue Thr-728 is with a Ser residue; (xiv) the amino acid substitution at the position corresponding with amino acid residue Met-732 is with a Leu residue; (xv) the amino acid substitution at the position corresponding with amino acid residue Arg-741 is with a Ser, Ala, Pro, Gin, or Thr residue; (xvi) the amino acid substitution at the position corresponding with amino acid residue Asn-743 is with a Ser, Thr, or Asp residue; (xvii) the amino acid substitution at the position corresponding with amino acid residue Ala-777 is with an Asn residue; (xviii) the amino acid substitution at the position corresponding with amino acid residue Tyr-848 is with a Glu residue; and/or (xix) the amino acid substitution at the position corresponding with amino acid residue Ile-1453 is with a Gly or Met residue.

3. The non-native glucosyltransferase of embodiment 1 or 2, comprising at least one amino acid substitution at a position corresponding with amino acid residue Gln-588, Arg-741, or Arg-722 of SEQ ID NO:62; optionally wherein: (i) the amino acid substitution at the position corresponding with amino acid residue Gln-588 is with a Leu residue; (ii) the amino acid substitution at the position corresponding with amino acid residue Arg-741 is with a Ser residue; and/or (iii) the amino acid substitution at the position corresponding with amino acid residue Arg-722 is with a His residue.

4. The non-native glucosyltransferase of embodiment 3, comprising two or more amino acid substitutions at positions corresponding with amino acid residues Gln-588, Arg-741, or Arg-722 of SEQ ID NO:62.

5. The non-native glucosyltransferase of embodiment 1, 2, 3, or 4, wherein the insoluble alpha-glucan produced by the non-native glucosyltransferase comprises at least about 50% alpha-1,3 linkages, and optionally wherein it has a weight average degree of polymerization (DP_w) of at least 100.

6. The non-native glucosyltransferase of embodiment 1, 2, 3, 4, or 5, wherein the insoluble alpha-glucan produced by the non-native glucosyltransferase has a DP_w of at least 650.

7. The non-native glucosyltransferase of embodiment 5 or 6, comprising a catalytic domain that is at least about 90% identical to residues 55-960 of SEQ ID NO:4, residues

54-957 of SEQ ID NO:65, residues 55-960 of SEQ ID NO:30, residues 55-960 of SEQ ID NO:28, or residues 55-960 of SEQ ID NO:20.

8. The non-native glucosyltransferase of embodiment 5, 6, or 7, comprising an amino acid sequence that is at least about 90% identical to SEQ ID NO:4, SEQ ID NO:65, SEQ ID NO:30, SEQ ID NO:28, or SEQ ID NO:20.

9. The non-native glucosyltransferase of embodiment 1, 2, 3, 4, 5, 6, 7, or 8, wherein the insoluble alpha-glucan produced by the non-native glucosyltransferase comprises at least about 90% (or at least 95%) alpha-1,3 linkages.

10. The non-native glucosyltransferase of embodiment 1, 2, 3, 4, 5, 6, 7, 8, or 9, wherein the molecular weight of the insoluble alpha-glucan produced by the non-native glucosyltransferase is at least about 10% higher than the molecular weight of insoluble alpha-glucan synthesized by the second glucosyltransferase.

11. A polynucleotide comprising a nucleotide sequence encoding a non-native glucosyltransferase according to any one of embodiments 1-10, optionally wherein one or more regulatory sequences are operably linked to the nucleotide sequence, and preferably wherein the one or more regulatory sequences include a promoter sequence.

12. A reaction composition comprising water, sucrose, and a non-native glucosyltransferase according to any one of embodiments 1-10.

13. A method of producing insoluble alpha-glucan comprising: (a) contacting at least water, sucrose, and a non-native glucosyltransferase enzyme according to any one of embodiments 1-10, whereby insoluble alpha-glucan is produced; and (b) optionally, isolating the insoluble alpha-glucan produced in step (a).

14. A method of preparing a polynucleotide sequence encoding a non-native glucosyltransferase (e.g., of any one of embodiments 1-10), the method comprising: (a) identifying a polynucleotide sequence encoding a parent glucosyltransferase that (i) comprises an amino acid sequence that is at least about 40% identical to SEQ ID NO:4 or positions 55-960 of SEQ ID NO:4, and (ii) synthesizes insoluble alpha-glucan comprising 1,3-linkages; and (b) modifying the polynucleotide sequence identified in step (a) to substitute at least one amino acid of the parent glucosyltransferase at a position corresponding with amino acid residue Asn-531, Arg-534, Thr-563, Glu-567, Val-586, Gln-588, Ile-591, Lys-593, Ile-608, Ala-610, Leu-661, Arg-722, Thr-728, Met-732, Arg-741, Asn-743, Ala-777, Tyr-848, or Ile-1453 of SEQ ID NO:62, thereby providing a polynucleotide sequence encoding a non-native glucosyltransferase that synthesizes insoluble alpha-glucan with a molecular weight that is higher than the molecular weight of insoluble alpha-glucan synthesized by the parent glucosyltransferase.

15. The method of embodiment 14, wherein the identifying step is performed: (a) in silico, (b) with a method comprising a nucleic acid hybridization step, (c) with a method comprising a protein sequencing step, and/or (d) with a method comprising a protein binding step; and/or wherein the modifying step is performed: (e) in silico, followed by synthesis of the polynucleotide sequence encoding the non-native glucosyltransferase enzyme, or (f) using a physical copy of the polynucleotide sequence encoding the parent glucosyltransferase.

EXAMPLES

[0114] The present disclosure is further exemplified in the following Examples. It should be understood that these Examples, while indicating certain preferred aspects herein, are given by way of illustration only. From the above discussion and these Examples, one skilled in the art can ascertain the essential characteristics of the disclosed embodiments, and without departing from the spirit and scope thereof, can make various changes and modifications to adapt the disclosed embodiments to various uses and conditions.

Example 1

Analysis of Amino Acid Sites Affecting Glucosyltransferase Alpha-Glucan Product Molecular Weight

[0115] This Example describes screening for glucosyltransferase variants that produce alpha-glucan with increased molecular weight. This screening was performed using a site evaluation library (SEL).

[0116] The amino acid sequence of the glucosyltransferase used to prepare amino acid substitutions in this Example was SEQ ID NO:4 (GTF 6855), which essentially is an N-terminally truncated (signal peptide and variable region removed) version of the full-length wild type glucosyltransferase (represented by SEQ ID NO:62) from *Streptococcus salivarius* SK126 (see Table 1). Substitutions made in SEQ ID NO:4 can be characterized as substituting for native amino acid residues, as each amino acid residue/position of SEQ ID NO:4 (apart from the Met-1 residue of SEQ ID NO:4) corresponds accordingly with an amino acid residue/position within SEQ ID NO:62. In reactions comprising at least sucrose and water, the glucosyltransferase of SEQ ID NO:4 typically produces alpha-glucan having about 100% alpha-1,3 linkages and a DP_w of 400 or greater (e.g., refer to U.S. Pat. Nos. 8,871,474 and 9,169,506, and U.S. Pat. Appl. Publ. No. 2017/0002336, which are incorporated herein by reference). This alpha-glucan product, which is insoluble, can be isolated following enzymatic synthesis via filtration, for example.

[0117] To summarize this Example, GTF 6855 variants (each with a single amino acid substitution) from SELs were each bacterially expressed, purified, and normalized to a concentration of 100 ppm. Each enzyme preparation was then screened (in triplicate) using sucrose as substrate in alpha-1,3-glucan synthesis reactions. Alpha-1,3-glucan polymer obtained in each reaction was analyzed for length (DP_w) using size exclusion chromatography (SEC).

[0118] Plasmids for individually expressing various single amino acid-substituted variants of GTF 6855 (SEQ ID NO:4) in a *Bacillus subtilis* host were prepared. Such plasmids were prepared as follows. A DNA expression cassette having (operably linked in 5'-to-3' order) the *B. subtilis* aprE promoter, a codon-optimized sequence encoding SEQ ID NO:4 (GTF 6855), and a BPN' terminator was synthesized. This expression cassette was cloned into the pHYT replicating shuttle vector (forming pHYT-GTF6855) and transformed into *B. subtilis* CBS12-1. The pHYT vector was derived from pHY300PLK (Takara) by adding a terminator sequence (SEQ ID NO:67) after the tetracycline resistance gene using the BstEII and EcoRI sites. The HindIII site in pHY300PLK had been removed by cloning a linker

sequence (not shown) into the BamHI and HindIII sites. The pHYT-GTF6855 plasmid was amplified and used for generating SELs. The resulting plasmids encoding single-amino acid substituted GTFs were sequenced to verify each substitution.

[0119] To produce GTF 6855 (SEQ ID NO:4) and single amino acid-substituted variants thereof, *B. subtilis* individually transformed with pHYT-GTF6855 or mutated versions thereof were cultivated in Tryptone Soya Broth (Oxoid Ltd., UK) and Grant's II medium. Heart infusion agar plates (Difco Laboratories, MI) were used to select transformants. Plasmid integrity was maintained by the addition of 25 µg/mL tetracycline. Each GTF targeted for expression was detected in the growth medium after incubation for about 6 hours at 37° C. After centrifugation and filtration, culture supernatants with expressed GTF were obtained. GTF enzyme present in the supernatant was purified to apparent homogeneity by affinity chromatography using washed (2×MILLIQ 1×25 mM NaH₂PO₄ pH 5.7 with intermediate centrifugation steps 100×g) SUPERDEX 200 resin (GE Healthcare). Each GTF was eluted with a 15% solution of Dextran T1 (Pharmacosmos) in 25 mM NaH₂PO₄ pH 5.7 by centrifugation 100×g. Each purified GTF was dialyzed against 25 mM NaH₂PO₄ pH 5.7 buffer (at least 100×) using a Harvard Apparatus 96-well DISPODIALYZER (10000-Dalton MWCO).

[0120] After dialysis, GTF enzyme concentration was determined by OD280 using purified GTF 6855 as a standard. Normalization of each purified GTF to 100 ppm was achieved by diluting appropriately with 25 mM NaH₂PO₄ pH 5.7. Protein concentration for each sample was confirmed using an AGILENT 1200 (Agilent Technologies) HPLC equipped with an AGILENT BIO SEC3 guard-column column (3 µm 100 Å (4.6×50 mm). Five (5) µL of sample was injected onto the column for each determination. Compounds were eluted with isocratic flow of 25 mM KH₂PO₄ pH 6.8±0.1 M NaCl for 1.3 min at 0.5 mL/min flow rate.

[0121] Each GTF (GTF 6855 and each variant thereof) was entered into a reaction with sucrose to produce alpha-glucan. Each reaction was performed as follows: 37.5 µL of 100 ppm enzyme sample (ppm based on a BSA calibration curve) was added to 262.5 µL of 86 g/L sucrose (75 g/L final) in 20 mM Na₂HPO₄/NaH₂PO₄ pH 5.7 and incubated overnight (about 20 hours) at 30° C. After this incubation, each reaction was quenched by incubation for 1 hour at 80° C. Appropriate analyses indicated that each variant enzyme listed in Table 3 below was able to perform a glucosyltransferase reaction producing alpha-1,3-glucan (data not shown).

[0122] A 100-µL aliquot of each quenched reaction was diluted 20× in DMSO/2% LiCl and filtered via centrifugation through a 0.2-µm PALL GHP membrane (4000 g×30 min×30° C.) in preparation for SEC analysis. Alpha-1,3-glucan polymer size was approximated using a WATERS APC-SEC system equipped with a WATERS ACQUITY APC-XT 450-A 2.5-µm 4.6×30 mm column. The column was held at 55° C. with a flow-rate of 0.65 mL/min of DMSO/0.25% LiCl mobile-phase. Dextran analytical standards with molecular weights of 80, 165, 325 and 750 kD were used to approximate alpha-1,3-glucan DP_w's of 280, 480, 660 and 880, respectively, via elution peak apexes.

[0123] The molecular weight (DP_w) and polydispersity index (PDI) of alpha-1,3-glucan produced in each reaction (~20 hours) as measured via the above methodology are provided in Table 3.

TABLE 3

Insoluble Alpha-1,3-Glucan Produced by GTF 6855 (SEQ ID NO: 4) and Single Amino Acid-Substituted Variants thereof		
GTF	Alpha-1,3-Glucan	
	DP _w	PDI
Plate 1 ^a		
6855 ^b	611	2.2
6855 ^b	635	2.1
6855 ^b	633	2.1
6855 ^b	626	2.1
V186A ^c	589	2.0
V186M	580	2.0
E194C	580	2.3
L434N	613	2.2
A472C	530	1.8
A472S	374	2.2
A510E	654	2.0
A510I	621	2.1
A510V	655	2.1
M529L	558	2.1
R534G	711	2.2
R534I	789	2.3
R534L	763	2.3
R534M	776	2.2
G576H	436	2.3
Q588L	817	2.1
I591K	816	2.0
I591R	832	2.0
Y605W	524	1.9
F607N	561	2.0
F607W	624	2.0
A610C	799	2.4
N613I	555	2.1
N613M	587	2.1
N613T	526	2.0
N613V	578	2.0
K625A	638	2.3
K625M	623	2.2
A510E	622	2.0
S631T	532	2.1
T635H	539	2.1
T635W	528	2.1
I636H	521	2.1
Y848E	843	2.0
D947G	408	2.1
F951Y	325	2.0
E849M	610	2.4
Q1007A	394	1.9
D1003G	486	2.1
A1022M	303	1.8
D1028L	416	1.9
D1028Q	537	2.1
A1057H	624	2.3
N1096A	562	2.2
Y1104M	611	2.2
N1122K	614	2.3
E1132A	589	2.2
E1132H	611	2.2
E1132K	610	2.2
E1132R	622	2.1
V1135K	612	2.3
V1188E	641	2.2
L1212N	630	2.0
E1250R	606	2.0
T1381E	612	2.1
T1431M	625	2.0
A1442R	609	2.0
E1450F	611	2.0

TABLE 3-continued

Insoluble Alpha-1,3-Glucan Produced by GTF 6855 (SEQ ID NO: 4) and Single Amino Acid-Substituted Variants thereof		
GTF	Alpha-1,3-Glucan	
	DP _w	PDI
E1450W	618	2.0
Dead ^d		
Blank ^e		
Blank ^e		
Plate 2 ^a		
6855 ^b	622	2.1
6855 ^b	628	2.1
6855 ^b	634	2.1
6855 ^b	619	2.2
I1453M ^c	635	2.1
V1491F	604	2.0
P1499Y	587	2.0
Y219C	591	2.0
E243H	631	2.1
A377I	514	2.1
I411F	586	2.3
I411S	591	2.1
D425Q	681	2.1
L428V	577	2.0
M529N	560	2.1
N531G	977	2.2
G576R	416	1.8
Y580H	554	2.1
K593M	792	1.9
I608Y	708	1.9
N613G	644	2.0
N613L	618	2.0
D617E	419	2.1
E621T	603	2.1
I627W	506	2.2
S631D	521	2.0
S631E	545	2.0
S631R	521	2.1
G633W	493	2.2
F634A	523	2.1
T635E	561	2.2
T635I	648	2.1
T635Y	518	2.1
R722H	793	2.5
T728S	769	2.4
M732L	791	2.4
A777N	755	2.4
A510E	625	2.2
N904E	554	2.5
K930G	637	2.5
K930V	582	2.3
D947F	619	2.6
D947I	610	2.4
D947K	559	2.5
D947N	635	2.6
D947Q	635	2.9
D947S	603	2.7
D947V	621	2.5
D947Y	624	2.6
Q1007S	578	2.6
D1003N	570	2.6
I1026H	621	2.6
D1028A	568	2.1
D1028M	535	2.1
V1037A	591	2.2
K1041A	583	2.1
K1041M	648	2.3
D1080M	554	2.2
F1244P	589	2.2
F1244Q	534	1.9
E1250H	553	2.1
E1250K	591	2.2
T1431Q	663	2.2
E1450D	585	2.2

TABLE 3-continued

Insoluble Alpha-1,3-Glucan Produced by GTF 6855 (SEQ ID NO: 4) and Single Amino Acid-Substituted Variants thereof		
GTF	Alpha-1,3-Glucan	
	DP _w	PDI
G1484P	627	2.2
I1453G	881	2.1
W1437N	654	2.3
R722N	766	2.2
Dead ^d		
Blank ^e		
Blank ^e		

^aGlucan synthesis reactions were run in microtiter plate format (two plates).

^bGTF 6855, SEQ ID NO: 4. Reactions with this GTF were run in quadruplicate per plate.

^cEach listed GTF with a substitution is a version of GTF 6855 comprising a substitution at a respective position, where the position number is in correspondence with the residue numbering of SEQ ID NO: 62. The wild type residue is listed first (before residue position number) and the substituting residue is listed second (after the residue position number) (this "wild type residue-position number-variant residue" annotation format applies throughout the present disclosure).

^dGTF with destroyed activity was entered into the reaction. Alpha-1,3-glucan was not detected.

^eNo GTF was added to the reaction. Alpha-1,3-glucan was not detected.

[0124] Based on the data in Table 3, individual substitutions at amino acid positions Y848, I591, Q588, A610, R534, N531, I1453, K593, M732, T728, R722, A777, and I608, for example, in GTF 6855 (SEQ ID NO:4) each result in an enzyme that produces insoluble alpha-1,3-glucan with a DP_w at least 10% greater than the average DP_w of insoluble alpha-1,3-glucan produced by the parent non-substituted enzyme (GTF 6855, SEQ ID NO:4). Interestingly, these higher DP_w alpha-1,3-glucan products generally had a PDI that was the same as, or similar to, the average PDI (2.1-2.2) of alpha-1,3-glucan produced by the parent non-substituted enzyme (GTF 6855, SEQ ID NO:4), meaning that the increase in molecular weight likely did not compromise polymer uniformity.

[0125] In a similar SEL study (not all data shown), individual substitutions in GTF 6855 (SEQ ID NO:4) at the following amino acid positions appeared to also have an enhancing effect on insoluble alpha-1,3-glucan molecular weight (substituting residue, resulting DP_w): N614 (P, 1054), R609 (H, 1052), F424 (A, 1051; V, 1023; L, 942; E, 937; Q, 725), W511 (Y, 1020), N475 (Q, 975; S, 954), A610 (T, 972; C, 959), Y848 (E, 922), N1214 (L, 918; I, 863), N531 (L, 879; M, 724; G, 714), I591 (K, 840; R, 824), R534 (K, 759), Q588 (L, 734), and R722 (H, 701) (non-substituted GTF 6855 produced insoluble alpha-1,3-glucan with DP_w 487).

[0126] One or more substitutions at any of the foregoing sites in this example are expected to allow for production of insoluble alpha-1,3-glucan with a DP_w significantly higher than the DP_w of alpha-1,3-glucan produced by a parent non-substituted glucosyltransferase.

Example 2

Generating Glucosyltransferase Variants that Produce Alpha-Glucan Products of Higher Molecular Weight

[0127] This Example describes another screening for glucosyltransferase variants that produce alpha-glucan with increased molecular weight.

[0128] Saturation mutagenesis was performed on GTF 6855 (SEQ ID NO:4) to provide a multitude of single amino acid-substituted variants of this glucosyltransferase. Each

variant was entered into a glucan synthesis reaction with parameters that were the same as, or similar to, the following: vessel, 250-mL bottom-indented shake flask agitated at 120 rpm; initial pH, 5.7; reaction volume, 50 mL; sucrose, 75 g/L; GTF, 1.5 mL lysate of *E. coli* cells heterologously expressing enzyme; KH_2PO_4 , 5 mM; temperature, 30° C.; time, about 20 hours. The molecular weight (DP_w) of alpha-1,3-glucan produced in each reaction (as measured via SEC methodology similar to that disclosed in Example 1) is provided in Table 4.

TABLE 4

Molecular Weight of Insoluble Alpha-1,3-Glucan Produced by GTF 6855 (SEQ ID NO: 4) and Single Amino Acid-Substituted Variants thereof	
GTF	Alpha-1,3-Glucan DP_w
6855 ^a	558
E567Q	1001
I591V	859
L661P	842
N743D	700
N743S	937
N743T	874
R741A	831
R741P	871
R741Q	886
R741S	887
R741T	693
T563A	910
V586T	874

^aGTF 6855, SEQ ID NO: 4. The reaction with this GTF was performed separately under the same conditions as described above.

[0129] Based on the data in Table 4, it is apparent, for example, that each listed single amino acid substitution in GTF 6855 (SEQ ID NO:4) results in an enzyme that produces insoluble alpha-1,3-glucan with increased molecular weight (DP_w). Thus, one or more substitutions at the positions indicated in Table 4 are expected to allow for production of insoluble alpha-1,3-glucan with a DP_w significantly higher than the DP_w of alpha-1,3-glucan produced by a parent non-substituted glucosyltransferase.

Example 3

Analysis of the Effects of Amino Acid Substitution Combinations on Glucosyltransferase Alpha-Glucan Synthesis Activity

[0130] This Example describes the effects of introducing multiple amino acid substitutions to a glucosyltransferase

and determining their effect on its alpha-glucan synthesis function. This analysis indicates, for example, that amino acid substitutions identified above to enhance alpha-glucan product molecular weight can be included in substitution combinations that likewise impart this molecular weight enhancement.

[0131] Briefly, certain combinations of amino acid substitutions were made to SEQ ID NO:4 (GTF 6855, see Table 1 and Example 1 for description of this glucosyltransferase) by site-directed mutagenesis of appropriate DNA templates contained in a plasmid. The plasmid sequences encoding each modified glucosyltransferase were individually sequenced to confirm the intended codon changes. Each combination of substitutions is listed in Table 5 below; appropriate analyses indicated that each modified enzyme was able to perform a glucosyltransferase reaction producing alpha-1,3-glucan (data not shown).

[0132] Expression plasmids encoding the modified glucosyltransferases were individually used to transform a *B. subtilis* strain containing nine protease deletions (amyE::xylRPxylAcomK-ermC, degUHy32, oppA, $\Delta\text{spoIIE3501}$, ΔaprE , ΔnprE , Δepr , ΔispA , Δbpr , Δvpr , ΔwprA , $\Delta\text{mpr-ybfJ}$, ΔnprB). Transformed cells were spread onto LB plates supplemented with 5 $\mu\text{g/mL}$ chloramphenicol. Colonies growing on these plates were streaked several times onto LB plates with 25 $\mu\text{g/mL}$ chloramphenicol. Each resulting *Bacillus* strain for expressing a particular variant glucosyltransferase was then grown for 6-8 hours in LB medium containing 25 $\mu\text{g/mL}$ chloramphenicol, and then subcultured into Grants II medium at 30° C. for 2-3 days. The cultures were spun at 15000 g for 30 minutes at 4° C., and the supernatants were filtered through 0.22- μm filters. The filtered supernatants, each of which contained an expressed secreted variant glucosyltransferase, were aliquoted and frozen at -80° C., and later used (below) for analyzing alpha-1,3-glucan synthesis activity.

[0133] The same amount of each variant enzyme, activity-wise, was entered into a glucan synthesis reaction with parameters that were the same as, or similar to, the following: vessel, 500-mL jacketed reactor with Teflon®-pitched blade turbine (45-degree angle) on a glass stir rod and agitated at 50-200 rpm; initial pH, 5.5; reaction volume, 500 mL; sucrose, 108 g/L; KH_2PO_4 , 1 mM; temperature, 39° C.; time, about 18-24 hours; filtrate from a previous alpha-1,3-glucan synthesis reaction, 50 vol %. The molecular weight (DP_w) of alpha-1,3-glucan produced in each reaction (as measured via methodology similar to that disclosed in Example 1) is provided in Table 5.

TABLE 5

Alpha-1,3 Glucan Products of GTF 6855 (SEQ ID NO: 4) Variants with Multiple Amino Acid Substitutions												
GTF ^a										Alpha-1,3-Glucan ^b DP _w		
A510D	Q588L	F607Y	R741S	D948G			R722H	T877K	M1253I	K1277N	844	
A510D	Q588L	F607Y	R741S	D948G			R722H	T877K	V1188E	M1253I	Q957P	744
A510D	Q588L	F607Y	R741S	D948G				T877K	V1188E	M1253I	Q957P	812
A510D	Q588L	F607Y	R741S	D948G						M1253I		750
A510D	Q588L	F607W	R741S	D948G								752
	Q588L	F607Y	R741S	D948G								705
A510D	Q588L	F607Y	R741S	D948G	N628D	T635A		T877K		M1253I	F929L	855
A510D	Q588L	F607W	R741S	D948G	S631T	S710G	R722H	T877K	V1188E	M1253I		863
A510D	Q588L	F607W	R741S	D948G	S631T	S710G	R722H	T877K	V1188E			812
A510D	Q588L	F607W	R741S	D948G	S631T	S710G		T877K	V1188E	M1253I		727

TABLE 5-continued

Alpha-1,3 Glucan Products of GTF 6855 (SEQ ID NO: 4) Variants with Multiple Amino Acid Substitutions											Alpha-1,3-Glucan ^b DP _w
GTF ^a											
A510D	Q588L	F607Y	R741S	D948G							697
A510D	Q588L	F607Y	R741S	D948G					V1188E		703
A510D	Q588L	F607W	R741S	D948G	S631T	S710G			V1188E		676
A510D	Q588L	F607W	R741S	D948G		S710G	R722H	T877K		M1253I	963
A510D	Q588L	F607Y	R741S	D948G	S631T		R722H	T877K	V1188E	M1253I	906
A510D	Q588L	F607W	R741S	D948G	S631T			T877K	V1188E	M1253I	781
A510D	Q588L	F607W	R741S	D948G	S631T				V1188E		687
A510D	Q588L	F607Y	R741S	D948G	S631T		R722H	T877K	V1188E	M1253I	961
A510D	Q588L	F607W	R741S	D948G					V1188E	M1253I	781

^aEach listed GTF is a version of GTF 6855 (SEQ ID NO: 4) comprising substitutions at respective positions, where each position number is in correspondence with the residue numbering of SEQ ID NO: 62.

^bInsoluble alpha-1,3-glucan product.

[0134] Based on the data in Table 5, it is apparent that introduction of multiple amino acid substitutions to GTF 6855 (SEQ ID NO:4), including substitutions that enhance molecular weight, can be employed in efforts to produce higher molecular weight insoluble alpha-1,3-glucan; for example, compare these DP_w values to those of GTF 6855 (SEQ ID NO:4) without substitutions shown in Table 3.

[0135] It is apparent, for example, that a glucosyltransferase with multiple substitutions, including those at positions corresponding to positions Gln-588, Arg-741, and/or Arg-722 of SEQ ID NO:62, can increase the molecular weight of insoluble alpha-glucan produced by the glucosyltransferase.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 67

<210> SEQ ID NO 1

<211> LENGTH: 4308

<212> TYPE: DNA

<213> ORGANISM: *Streptococcus sobrinus*

<400> SEQUENCE: 1

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gcagacagct ggtatcgctc gaaatccatc ctgaaggacg gcaaacctg gaccgagagc     300
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aactacgtga actatatgaa taaagtggtc ggtattgaca agacgtacac tgcggaaaacg     420
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-continued

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gcacatgata gcgaggtgca ggacatcatc cgtgacatta tcaaggctga gattaaccca	1260
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<210> SEQ ID NO 2

<211> LENGTH: 1435

<212> TYPE: PRT

<213> ORGANISM: Streptococcus sobrinus

<400> SEQUENCE: 2

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Trp Pro Asp Thr Glu Thr Lys Arg Asn Tyr Val Asn Tyr Met Asn Lys
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Leu Thr Ala Ala Ala Glu Leu Val Gln Ala Arg Ile Glu Gln Lys Ile
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Thr Ser Glu Asn Asn Thr Lys Trp Leu Arg Glu Ala Ile Ser Ala Phe
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<212> TYPE: DNA

<213> ORGANISM: Streptococcus salivarius SK126

<400> SEQUENCE: 3

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gacggttcgc aagtgaaggg cgggtgtggc aagaacggcg atggcaccta tagcaaatat	3720
gatgcgtcta ccggcgaaac cctgaccaat gagtttttca ccacgggtga taacaactgg	3780
tactacattg gcgcaaacgg caagagcgtg acgggcgagg tcaagatcgg tgacgatacc	3840
tatttctttg ccaaagatgg caagcaagtt aagggtcaaa ctgtcagcgc gggtaacggg	3900
cgtattagct actactatgg tgatagcggg aagcgtgcgg tgagcaactg gatcgaaatc	3960

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aattaa 4026

<210> SEQ ID NO 4

<211> LENGTH: 1341

<212> TYPE: PRT

<213> ORGANISM: Streptococcus salivarius SK126

<400> SEQUENCE: 4

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Glu Asn Phe Ala Ile Thr Val Asn Gly Gln Leu Leu Tyr Phe Gly Lys
20 25 30

Asp Gly Ala Leu Thr Ser Ser Ser Thr Tyr Ser Phe Thr Pro Gly Thr
35 40 45

Thr Asn Ile Val Asp Gly Phe Ser Ile Asn Asn Arg Ala Tyr Asp Ser
50 55 60

Ser Glu Ala Ser Phe Glu Leu Ile Asp Gly Tyr Leu Thr Ala Asp Ser
65 70 75 80

Trp Tyr Arg Pro Ala Ser Ile Ile Lys Asp Gly Val Thr Trp Gln Ala
85 90 95

Ser Thr Ala Glu Asp Phe Arg Pro Leu Leu Met Ala Trp Trp Pro Asn
100 105 110

Val Asp Thr Gln Val Asn Tyr Leu Asn Tyr Met Ser Lys Val Phe Asn
115 120 125

Leu Asp Ala Lys Tyr Ser Ser Thr Asp Lys Gln Glu Thr Leu Lys Val
130 135 140

Ala Ala Lys Asp Ile Gln Ile Lys Ile Glu Gln Lys Ile Gln Ala Glu
145 150 155 160

Lys Ser Thr Gln Trp Leu Arg Glu Thr Ile Ser Ala Phe Val Lys Thr
165 170 175

Gln Pro Gln Trp Asn Lys Glu Thr Glu Asn Tyr Ser Lys Gly Gly Gly
180 185 190

Glu Asp His Leu Gln Gly Gly Ala Leu Leu Tyr Val Asn Asp Ser Arg
195 200 205

Thr Pro Trp Ala Asn Ser Asp Tyr Arg Arg Leu Asn Arg Thr Ala Thr
210 215 220

Asn Gln Thr Gly Thr Ile Asp Lys Ser Ile Leu Asp Glu Gln Ser Asp
225 230 235 240

Pro Asn His Met Gly Gly Phe Asp Phe Leu Leu Ala Asn Asp Val Asp
245 250 255

Leu Ser Asn Pro Val Val Gln Ala Glu Gln Leu Asn Gln Ile His Tyr
260 265 270

Leu Met Asn Trp Gly Ser Ile Val Met Gly Asp Lys Asp Ala Asn Phe
275 280 285

Asp Gly Ile Arg Val Asp Ala Val Asp Asn Val Asp Ala Asp Met Leu
290 295 300

Gln Leu Tyr Thr Asn Tyr Phe Arg Glu Tyr Tyr Gly Val Asn Lys Ser
305 310 315 320

Glu Ala Asn Ala Leu Ala His Ile Ser Val Leu Glu Ala Trp Ser Leu
325 330 335

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Asn	Asp	Asn	His	Tyr	Asn	Asp	Lys	Thr	Asp	Gly	Ala	Ala	Leu	Ala	Met
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Glu	Asn	Lys	Gln	Arg	Leu	Ala	Leu	Leu	Phe	Ser	Leu	Ala	Lys	Pro	Ile
		355					360					365			
Lys	Glu	Arg	Thr	Pro	Ala	Val	Ser	Pro	Leu	Tyr	Asn	Asn	Thr	Phe	Asn
	370					375					380				
Thr	Thr	Gln	Arg	Asp	Glu	Lys	Thr	Asp	Trp	Ile	Asn	Lys	Asp	Gly	Ser
385					390					395					400
Lys	Ala	Tyr	Asn	Glu	Asp	Gly	Thr	Val	Lys	Gln	Ser	Thr	Ile	Gly	Lys
			405						410					415	
Tyr	Asn	Glu	Lys	Tyr	Gly	Asp	Ala	Ser	Gly	Asn	Tyr	Val	Phe	Ile	Arg
		420						425					430		
Ala	His	Asp	Asn	Asn	Val	Gln	Asp	Ile	Ile	Ala	Glu	Ile	Ile	Lys	Lys
		435					440					445			
Glu	Ile	Asn	Pro	Lys	Ser	Asp	Gly	Phe	Thr	Ile	Thr	Asp	Ala	Glu	Met
	450					455					460				
Lys	Gln	Ala	Phe	Glu	Ile	Tyr	Asn	Lys	Asp	Met	Leu	Ser	Ser	Asp	Lys
465					470					475					480
Lys	Tyr	Thr	Leu	Asn	Asn	Ile	Pro	Ala	Ala	Tyr	Ala	Val	Met	Leu	Gln
			485						490					495	
Asn	Met	Glu	Thr	Ile	Thr	Arg	Val	Tyr	Tyr	Gly	Asp	Leu	Tyr	Thr	Asp
		500						505					510		
Asp	Gly	His	Tyr	Met	Glu	Thr	Lys	Ser	Pro	Tyr	Tyr	Asp	Thr	Ile	Val
		515					520					525			
Asn	Leu	Met	Lys	Ser	Arg	Ile	Lys	Tyr	Val	Ser	Gly	Gly	Gln	Ala	Gln
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Arg	Ser	Tyr	Trp	Leu	Pro	Thr	Asp	Gly	Lys	Met	Asp	Asn	Ser	Asp	Val
545					550					555					560
Glu	Leu	Tyr	Arg	Thr	Asn	Glu	Val	Tyr	Thr	Ser	Val	Arg	Tyr	Gly	Lys
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Asp	Ile	Met	Thr	Ala	Asn	Asp	Thr	Glu	Gly	Ser	Lys	Tyr	Ser	Arg	Thr
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Ser	Gly	Gln	Val	Thr	Leu	Val	Ala	Asn	Asn	Pro	Lys	Leu	Thr	Leu	Asp
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Gln	Ser	Ala	Lys	Leu	Asn	Val	Glu	Met	Gly	Lys	Ile	His	Ala	Asn	Gln
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Lys	Tyr	Arg	Ala	Leu	Ile	Val	Gly	Thr	Ala	Asp	Gly	Ile	Lys	Asn	Phe
625					630					635					640
Thr	Ser	Asp	Ala	Asp	Ala	Ile	Ala	Ala	Gly	Tyr	Val	Lys	Glu	Thr	Asp
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Ser	Asn	Gly	Val	Leu	Thr	Phe	Gly	Ala	Asn	Asp	Ile	Lys	Gly	Tyr	Glu
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Thr	Phe	Asp	Met	Ser	Gly	Phe	Val	Ala	Val	Trp	Val	Pro	Val	Gly	Ala
		675					680					685			
Ser	Asp	Asp	Gln	Asp	Ile	Arg	Val	Ala	Pro	Ser	Thr	Glu	Ala	Lys	Lys
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Glu	Gly	Glu	Leu	Thr	Leu	Lys	Ala	Thr	Glu	Ala	Tyr	Asp	Ser	Gln	Leu
705					710					715					720
Ile	Tyr	Glu	Gly	Phe	Ser	Asn	Phe	Gln	Thr	Ile	Pro	Asp	Gly	Ser	Asp
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Pro	Ser	Val	Tyr	Thr	Asn	Arg	Lys	Ile	Ala	Glu	Asn	Val	Asp	Leu	Phe

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740					745					750					
Lys	Ser	Trp	Gly	Val	Thr	Ser	Phe	Glu	Met	Ala	Pro	Gln	Phe	Val	Ser
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Ala	Asp	Asp	Gly	Thr	Phe	Leu	Asp	Ser	Val	Ile	Gln	Asn	Gly	Tyr	Ala
	770						775				780				
Phe	Ala	Asp	Arg	Tyr	Asp	Leu	Ala	Met	Ser	Lys	Asn	Asn	Lys	Tyr	Gly
	785				790					795					800
Ser	Lys	Glu	Asp	Leu	Arg	Asp	Ala	Leu	Lys	Ala	Leu	His	Lys	Ala	Gly
			805						810					815	
Ile	Gln	Ala	Ile	Ala	Asp	Trp	Val	Pro	Asp	Gln	Ile	Tyr	Gln	Leu	Pro
		820						825					830		
Gly	Lys	Glu	Val	Val	Thr	Ala	Thr	Arg	Thr	Asp	Gly	Ala	Gly	Arg	Lys
		835					840					845			
Ile	Ala	Asp	Ala	Ile	Ile	Asp	His	Ser	Leu	Tyr	Val	Ala	Asn	Thr	Lys
	850					855					860				
Ser	Ser	Gly	Lys	Asp	Tyr	Gln	Ala	Lys	Tyr	Gly	Gly	Glu	Phe	Leu	Ala
	865				870					875					880
Glu	Leu	Lys	Ala	Lys	Tyr	Pro	Glu	Met	Phe	Lys	Val	Asn	Met	Ile	Ser
			885						890					895	
Thr	Gly	Lys	Pro	Ile	Asp	Asp	Ser	Val	Lys	Leu	Lys	Gln	Trp	Lys	Ala
		900						905					910		
Glu	Tyr	Phe	Asn	Gly	Thr	Asn	Val	Leu	Glu	Arg	Gly	Val	Gly	Tyr	Val
		915					920					925			
Leu	Ser	Asp	Glu	Ala	Thr	Gly	Lys	Tyr	Phe	Thr	Val	Thr	Lys	Asp	Gly
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Asn	Phe	Ile	Pro	Leu	Gln	Leu	Thr	Gly	Asn	Glu	Lys	Val	Val	Thr	Gly
	945				950					955					960
Phe	Ser	Asn	Asp	Gly	Lys	Gly	Ile	Thr	Tyr	Phe	Gly	Thr	Ser	Gly	Thr
			965					970						975	
Gln	Ala	Lys	Ser	Ala	Phe	Val	Thr	Phe	Asn	Gly	Asn	Thr	Tyr	Tyr	Phe
		980						985					990		
Asp	Ala	Arg	Gly	His	Met	Val	Thr	Asn	Gly	Glu	Tyr	Ser	Pro	Asn	Gly
	995						1000						1005		
Lys	Asp	Val	Tyr	Arg	Phe	Leu	Pro	Asn	Gly	Ile	Met	Leu	Ser	Asn	
	1010					1015					1020				
Ala	Phe	Tyr	Val	Asp	Ala	Asn	Gly	Asn	Thr	Tyr	Leu	Tyr	Asn	Ser	
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Lys	Gly	Gln	Met	Tyr	Lys	Gly	Gly	Tyr	Thr	Lys	Phe	Asp	Val	Thr	
	1040					1045						1050			
Glu	Thr	Asp	Lys	Asp	Gly	Lys	Glu	Ser	Lys	Val	Val	Lys	Phe	Arg	
	1055					1060						1065			
Tyr	Phe	Thr	Asn	Glu	Gly	Val	Met	Ala	Lys	Gly	Val	Thr	Val	Ile	
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Asp	Gly	Phe	Thr	Gln	Tyr	Phe	Gly	Glu	Asp	Gly	Phe	Gln	Ala	Lys	
	1085					1090					1095				
Asp	Lys	Leu	Val	Thr	Phe	Lys	Gly	Lys	Thr	Tyr	Tyr	Phe	Asp	Ala	
	1100					1105						1110			
His	Thr	Gly	Asn	Ala	Ile	Lys	Asp	Thr	Trp	Arg	Asn	Ile	Asn	Gly	
	1115					1120						1125			
Lys	Trp	Tyr	His	Phe	Asp	Ala	Asn	Gly	Val	Ala	Ala	Thr	Gly	Ala	
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Gln Val	Ile Asn Gly Gln Lys	Leu Tyr Phe Asn Glu	Asp Gly Ser
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Gln Val	Lys Gly Gly Val Val	Lys Asn Ala Asp Gly	Thr Tyr Ser
1160	1165	1170	
Lys Tyr	Lys Glu Gly Ser Gly	Glu Leu Val Thr Asn	Glu Phe Phe
1175	1180	1185	
Thr Thr	Asp Gly Asn Val Trp	Tyr Tyr Ala Gly Ala	Asn Gly Lys
1190	1195	1200	
Thr Val	Thr Gly Ala Gln Val	Ile Asn Gly Gln His	Leu Tyr Phe
1205	1210	1215	
Asn Ala	Asp Gly Ser Gln Val	Lys Gly Gly Val Val	Lys Asn Ala
1220	1225	1230	
Asp Gly	Thr Tyr Ser Lys Tyr	Asp Ala Ser Thr Gly	Glu Arg Leu
1235	1240	1245	
Thr Asn	Glu Phe Phe Thr Thr	Gly Asp Asn Asn Trp	Tyr Tyr Ile
1250	1255	1260	
Gly Ala	Asn Gly Lys Ser Val	Thr Gly Glu Val Lys	Ile Gly Asp
1265	1270	1275	
Asp Thr	Tyr Phe Phe Ala Lys	Asp Gly Lys Gln Val	Lys Gly Gln
1280	1285	1290	
Thr Val	Ser Ala Gly Asn Gly	Arg Ile Ser Tyr Tyr	Tyr Gly Asp
1295	1300	1305	
Ser Gly	Lys Arg Ala Val Ser	Thr Trp Ile Glu Ile	Gln Pro Gly
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Val Tyr	Val Tyr Phe Asp Lys	Asn Gly Ile Ala Tyr	Pro Pro Arg
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Val Leu	Asn		
1340			

<210> SEQ ID NO 5

<211> LENGTH: 3744

<212> TYPE: DNA

<213> ORGANISM: Streptococcus salivarius

<400> SEQUENCE: 5

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gggtgaactgt ctaatcagaa agagtatcgt ttcgacaaaa atggtggtagc tggtagcagc	180
gcggacagca cgaacaccaa cgtgactgtg aacggtgaca aaaacgcatt ttacggtacc	240
acggacaaaag acattgagct ggtcgacggc tatttcaccg cgaacacctg gtatcgcccc	300
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tctgaaaatc tggacaataa tgatcatctg caaggtggcg cctgctgta caataacgac	660
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<210> SEQ ID NO 6

<211> LENGTH: 1247

<212> TYPE: PRT

<213> ORGANISM: Streptococcus salivarius

<400> SEQUENCE: 6

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Ser Gln Tyr Phe Asn Ala Glu Thr Gly Glu Leu Ser Asn Gln Lys Glu
35          40          45
Tyr Arg Phe Asp Lys Asn Gly Gly Thr Gly Ser Ser Ala Asp Ser Thr
50          55          60
Asn Thr Asn Val Thr Val Asn Gly Asp Lys Asn Ala Phe Tyr Gly Thr
65          70          75          80
Thr Asp Lys Asp Ile Glu Leu Val Asp Gly Tyr Phe Thr Ala Asn Thr
85          90          95
Trp Tyr Arg Pro Lys Glu Ile Leu Lys Asp Gly Lys Glu Trp Thr Ala
100         105         110
Ser Thr Glu Asn Asp Lys Arg Pro Leu Leu Thr Val Trp Trp Pro Ser
115         120         125
Lys Ala Ile Gln Ala Ser Tyr Leu Asn Tyr Met Lys Glu Gln Gly Leu
130         135         140
Gly Thr Asn Gln Thr Tyr Thr Ser Phe Ser Ser Gln Thr Gln Met Asp
145         150         155         160
Gln Ala Ala Leu Glu Val Gln Lys Arg Ile Glu Glu Arg Ile Ala Arg
165         170         175
Glu Gly Asn Thr Asp Trp Leu Arg Thr Thr Ile Lys Asn Phe Val Lys
180         185         190
Thr Gln Pro Gly Trp Asn Ser Thr Ser Glu Asn Leu Asp Asn Asn Asp
195         200         205
His Leu Gln Gly Gly Ala Leu Leu Tyr Asn Asn Asp Ser Arg Thr Ser
210         215         220
His Ala Asn Ser Asp Tyr Arg Leu Leu Asn Arg Thr Pro Thr Ser Gln

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Phe	Glu	Phe	Leu	Leu	Ala	Asn	Asp	Ile	Asp	Asn	Ser	Asn	Pro	Ala	Val
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Gln	Ala	Glu	Gln	Leu	Asn	Trp	Leu	His	Tyr	Ile	Met	Asn	Ile	Gly	Thr
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Ile	Thr	Gly	Gly	Ser	Glu	Asp	Glu	Asn	Phe	Asp	Gly	Val	Arg	Val	Asp
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Ala	Val	Asp	Asn	Val	Asn	Ala	Asp	Leu	Leu	Gln	Ile	Ala	Ser	Asp	Tyr
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Phe	Lys	Ala	Lys	Tyr	Gly	Ala	Asp	Gln	Ser	Gln	Asp	Gln	Ala	Ile	Lys
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His	Leu	Ser	Ile	Leu	Glu	Ala	Trp	Ser	His	Asn	Asp	Ala	Tyr	Tyr	Asn
			340					345					350		
Glu	Asp	Thr	Lys	Gly	Ala	Gln	Leu	Pro	Met	Asp	Asp	Pro	Met	His	Leu
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Ala	Leu	Val	Tyr	Ser	Leu	Leu	Arg	Pro	Ile	Gly	Asn	Arg	Ser	Gly	Val
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Glu	Pro	Leu	Ile	Ser	Asn	Ser	Leu	Asn	Asp	Arg	Ser	Glu	Ser	Gly	Lys
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Asn	Ser	Lys	Arg	Met	Ala	Asn	Tyr	Ala	Phe	Val	Arg	Ala	His	Asp	Ser
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Glu	Val	Gln	Ser	Ile	Ile	Gly	Gln	Ile	Ile	Lys	Asn	Glu	Ile	Asn	Pro
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Gln	Ser	Thr	Gly	Asn	Thr	Phe	Thr	Leu	Asp	Glu	Met	Lys	Lys	Ala	Phe
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Glu	Ile	Tyr	Asn	Lys	Asp	Met	Arg	Ser	Ala	Asn	Lys	Gln	Tyr	Thr	Gln
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Tyr	Asn	Ile	Pro	Ser	Ala	Tyr	Ala	Leu	Met	Leu	Thr	His	Lys	Asp	Thr
465					470					475					480
Val	Pro	Arg	Val	Tyr	Tyr	Gly	Asp	Met	Tyr	Thr	Asp	Asp	Gly	Gln	Tyr
				485					490					495	
Met	Ala	Gln	Lys	Ser	Pro	Tyr	Tyr	Asp	Ala	Ile	Glu	Thr	Leu	Leu	Lys
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Gly	Arg	Ile	Arg	Tyr	Ala	Ala	Gly	Gly	Gln	Asp	Met	Lys	Val	Asn	Tyr
		515					520					525			
Ile	Gly	Tyr	Gly	Asn	Thr	Asn	Gly	Trp	Asp	Ala	Ala	Gly	Val	Leu	Thr
	530					535						540			
Ser	Val	Arg	Tyr	Gly	Thr	Gly	Ala	Asn	Ser	Ala	Ser	Asp	Thr	Gly	Thr
545					550					555					560
Ala	Glu	Thr	Arg	Asn	Gln	Gly	Met	Ala	Val	Ile	Val	Ser	Asn	Gln	Pro
				565					570					575	
Ala	Leu	Arg	Leu	Thr	Ser	Asn	Leu	Thr	Ile	Asn	Met	Gly	Ala	Ala	His
			580					585					590		
Arg	Asn	Gln	Ala	Tyr	Arg	Pro	Leu	Leu	Leu	Thr	Thr	Asn	Asp	Gly	Val
		595					600					605			
Ala	Thr	Tyr	Leu	Asn	Asp	Ser	Asp	Ala	Asn	Gly	Ile	Val	Lys	Tyr	Thr
	610					615					620				
Asp	Gly	Asn	Gly	Asn	Leu	Thr	Phe	Ser	Ala	Asn	Glu	Ile	Arg	Gly	Ile
625					630					635					640

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Arg	Asn	Pro	Gln	Val	Asp	Gly	Tyr	Leu	Ala	Val	Trp	Val	Pro	Val	Gly	645	650	655
Ala	Ser	Glu	Asn	Gln	Asp	Val	Arg	Val	Ala	Pro	Ser	Lys	Glu	Lys	Asn	660	665	670
Ser	Ser	Gly	Leu	Val	Tyr	Glu	Ser	Asn	Ala	Ala	Leu	Asp	Ser	Gln	Val	675	680	685
Ile	Tyr	Glu	Gly	Phe	Ser	Asn	Phe	Gln	Asp	Phe	Val	Gln	Asn	Pro	Ser	690	695	700
Gln	Tyr	Thr	Asn	Lys	Lys	Ile	Ala	Glu	Asn	Ala	Asn	Leu	Phe	Lys	Ser	705	710	715
Trp	Gly	Ile	Thr	Ser	Phe	Glu	Phe	Ala	Pro	Gln	Tyr	Val	Ser	Ser	Asp	725	730	735
Asp	Gly	Ser	Phe	Leu	Asp	Ser	Val	Ile	Gln	Asn	Gly	Tyr	Ala	Phe	Thr	740	745	750
Asp	Arg	Tyr	Asp	Ile	Gly	Met	Ser	Lys	Asp	Asn	Lys	Tyr	Gly	Ser	Leu	755	760	765
Ala	Asp	Leu	Lys	Ala	Ala	Leu	Lys	Ser	Leu	His	Ala	Val	Gly	Ile	Ser	770	775	780
Ala	Ile	Ala	Asp	Trp	Val	Pro	Asp	Gln	Ile	Tyr	Asn	Leu	Pro	Gly	Asp	785	790	795
Glu	Val	Val	Thr	Ala	Thr	Arg	Val	Asn	Asn	Tyr	Gly	Glu	Thr	Lys	Asp	805	810	815
Gly	Ala	Ile	Ile	Asp	His	Ser	Leu	Tyr	Ala	Ala	Lys	Thr	Arg	Thr	Phe	820	825	830
Gly	Asn	Asp	Tyr	Gln	Gly	Lys	Tyr	Gly	Gly	Ala	Phe	Leu	Asp	Glu	Leu	835	840	845
Lys	Arg	Leu	Tyr	Pro	Gln	Ile	Phe	Asp	Arg	Val	Gln	Ile	Ser	Thr	Gly	850	855	860
Lys	Arg	Met	Thr	Thr	Asp	Glu	Lys	Ile	Thr	Gln	Trp	Ser	Ala	Lys	Tyr	865	870	875
Met	Asn	Gly	Thr	Asn	Ile	Leu	Asp	Arg	Gly	Ser	Glu	Tyr	Val	Leu	Lys	885	890	895
Asn	Gly	Leu	Asn	Gly	Tyr	Tyr	Gly	Thr	Asn	Gly	Gly	Lys	Val	Ser	Leu	900	905	910
Pro	Lys	Val	Val	Gly	Ser	Asn	Gln	Ser	Thr	Asn	Gly	Asp	Asn	Gln	Asn	915	920	925
Gly	Asp	Gly	Ser	Gly	Lys	Phe	Glu	Lys	Arg	Leu	Phe	Ser	Val	Arg	Tyr	930	935	940
Arg	Tyr	Asn	Asn	Gly	Gln	Tyr	Ala	Lys	Asn	Ala	Phe	Ile	Lys	Asp	Asn	945	950	955
Asp	Gly	Asn	Val	Tyr	Tyr	Phe	Asp	Asn	Ser	Gly	Arg	Met	Ala	Val	Gly	965	970	975
Glu	Lys	Thr	Ile	Asp	Gly	Lys	Gln	Tyr	Phe	Phe	Leu	Ala	Asn	Gly	Val	980	985	990
Gln	Leu	Arg	Asp	Gly	Tyr	Arg	Gln	Asn	Arg	Arg	Gly	Gln	Val	Phe	Tyr	995	1000	1005
Tyr	Asp	Gln	Asn	Gly	Val	Leu	Asn	Ala	Asn	Gly	Lys	Gln	Asp	Pro		1010	1015	1020
Lys	Pro	Asp	Asn	Asn	Asn	Asn	Ala	Ser	Gly	Arg	Asn	Gln	Phe	Val		1025	1030	1035

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Gln Ile	Gly Asn Asn Val	Trp	Ala Tyr Tyr Asp	Gly	Asn Gly Lys
1040		1045		1050	
Arg Val	Thr Gly His Gln Asn	Ile Asn Gly Gln	Glu	Leu Phe Phe	
1055		1060		1065	
Asp Asn	Asn Gly Val Gln Val	Lys Gly Arg Thr	Val	Asn Glu Asn	
1070		1075		1080	
Gly Ala	Ile Arg Tyr Tyr Asp	Ala Asn Ser Gly	Glu	Met Ala Arg	
1085		1090		1095	
Asn Arg	Phe Ala Glu Ile Glu	Pro Gly Val Trp	Ala	Tyr Phe Asn	
1100		1105		1110	
Asn Asp	Gly Thr Ala Val Lys	Gly Ser Gln Asn	Ile	Asn Gly Gln	
1115		1120		1125	
Asp Leu	Tyr Phe Asp Gln Asn	Gly Arg Gln Val	Lys	Gly Ala Leu	
1130		1135		1140	
Ala Asn	Val Asp Gly Asn Leu	Arg Tyr Tyr Asp	Val	Asn Ser Gly	
1145		1150		1155	
Glu Leu	Tyr Arg Asn Arg Phe	His Glu Ile Asp	Gly	Ser Trp Tyr	
1160		1165		1170	
Tyr Phe	Asp Gly Asn Gly Asn	Ala Val Lys Gly	Met	Val Asn Ile	
1175		1180		1185	
Asn Gly	Gln Asn Leu Leu Phe	Asp Asn Asn Gly	Lys	Gln Ile Lys	
1190		1195		1200	
Gly His	Leu Val Arg Val Asn	Gly Val Val Arg	Tyr	Phe Asp Pro	
1205		1210		1215	
Asn Ser	Gly Glu Met Ala Val	Asn Arg Trp Val	Glu	Val Ser Pro	
1220		1225		1230	
Gly Trp	Trp Val Tyr Phe Asp	Gly Glu Gly Arg	Gly	Gln Ile	
1235		1240		1245	

<210> SEQ ID NO 7

<211> LENGTH: 4434

<212> TYPE: DNA

<213> ORGANISM: Streptococcus salivarius

<400> SEQUENCE: 7

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gttctgacgc ctgcaaaaga aacgaacgca gtcgagactg cgaccaccac taacaccag	180
gcgacggcgg aggcggccac gaccgcgacc accgcggacg tcgcggtggc tgcggtgccg	240
aacaaagaag cggtcgttac cacggatgct cggcggttca cgaccgagaa agcgggaagaa	300
cagccggcta ccgttaaagc agaagtcgtc aatacggaa tgaaagcgcc ggaagcggct	360
ctgaaagaca gcgaggttga ggcagcgtg agcctgaaga acatcaagaa cattgatggc	420
aagtattact atgttaatga ggatggcagc cacaagaga atttcgttat taccgtgaat	480
ggccagctgc tgtacttttg taaagacggt gcgctgacgt cctctagcac gtattctttt	540
accccaggca ctaccaatat cgtggacggt tttagcatta acaaccgcgc ttacgacagc	600
agcgaggcga gctttgagct gatcgacggt tacttgaccg cagacagctg gtatcgtccg	660
gctagcatca tcaaagatgg tgttacgtgg caagcgtcca ccgccgagga ttttcgtccg	720
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tggtgcgtg	aaactatcag	cgcctttgtg	aaaaccacgc	cgcagtggaa	caaagaaacc	960
gagaattaca	gcaaggggtg	tggtgaggac	cacctgcaag	gtggcgcact	gctgtatgtt	1020
aacgacagcc	gtaccccttg	ggcgaatagc	gattaccgtc	gtctgaatcg	caccgcaacc	1080
aatcagacgg	gcacgatcga	taagtctatt	ctggacgagc	agtctgaccc	aaaccacatg	1140
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gagcagctga	atcaaatcca	ctatctgatg	aattgggggt	ccattgtgat	gggtgacaag	1260
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caactgtata	ccaattactt	ccgtgagtag	tacggtgtga	acaagagcga	agctaacgca	1380
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gataccatcg	tgaatttgat	gaagagccgt	atcaagtatg	tttcgggtgg	ccaggcgcaa	2040
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gtcaagttcc gctactttac gaacgaaggc gtcattggcca aggggtgttac cgtcattgat 3660
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<210> SEQ ID NO 8

<211> LENGTH: 1477

<212> TYPE: PRT

<213> ORGANISM: Streptococcus salivarius

<400> SEQUENCE: 8

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Thr Ala Ser Leu Val Thr Ser Pro Glu Ala Thr Lys Glu Ala Asp Lys
20          25          30

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```

Arg Thr Asn Thr Lys Glu Ala Asp Val Leu Thr Pro Ala Lys Glu Thr
35          40          45

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```

Asn Ala Val Glu Thr Ala Thr Thr Thr Asn Thr Gln Ala Thr Ala Glu
50          55          60

```

```

Ala Ala Thr Thr Ala Thr Thr Ala Asp Val Ala Val Ala Ala Val Pro
65          70          75          80

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Asn Lys Glu Ala Val Thr Thr Asp Ala Pro Ala Val Thr Thr Glu
85          90          95

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```

Lys Ala Glu Glu Gln Pro Ala Thr Val Lys Ala Glu Val Val Asn Thr
100         105         110

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Glu Val Lys Ala Pro Glu Ala Ala Leu Lys Asp Ser Glu Val Glu Ala

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115					120					125					
Ala 130	Leu	Ser	Leu	Lys	Asn 135	Ile	Lys	Asn	Ile	Asp 140	Gly	Lys	Tyr	Tyr	Tyr
Val 145	Asn	Glu	Asp	Gly 150	Ser	His	Lys	Glu	Asn	Phe 155	Ala	Ile	Thr	Val	Asn 160
Gly	Gln	Leu	Leu	Tyr 165	Phe	Gly	Lys	Asp 170	Gly	Ala	Leu	Thr	Ser 175	Ser	Ser
Thr	Tyr	Ser	Phe 180	Thr	Pro	Gly	Thr	Thr 185	Asn	Ile	Val	Asp 190	Gly	Phe	Ser
Ile	Asn	Asn 195	Arg	Ala	Tyr	Asp 200	Ser	Ser	Glu	Ala	Ser	Phe 205	Glu	Leu	Ile
Asp 210	Gly	Tyr	Leu	Thr	Ala	Asp 215	Ser	Trp	Tyr	Arg	Pro 220	Ala	Ser	Ile	Ile
Lys 225	Asp	Gly	Val	Thr	Trp 230	Gln	Ala	Ser	Thr	Ala 235	Glu	Asp	Phe	Arg	Pro 240
Leu	Leu	Met	Ala	Trp 245	Trp	Pro	Asn	Val	Asp 250	Thr	Gln	Val	Asn	Tyr	Leu 255
Asn	Tyr	Met	Ser 260	Lys	Val	Phe	Asn	Leu	Asp 265	Ala	Lys	Tyr	Ser 270	Ser	Thr
Asp	Lys	Gln 275	Glu	Thr	Leu	Lys	Val	Ala	Ala 280	Lys	Asp	Ile 285	Gln	Ile	Lys
Ile	Glu	Gln 290	Lys	Ile	Gln	Ala 295	Glu	Lys	Ser	Thr	Gln 300	Trp	Leu	Arg	Glu
Thr 305	Ile	Ser	Ala	Phe	Val 310	Lys	Thr	Gln	Pro	Gln 315	Trp	Asn	Lys	Glu	Thr 320
Glu	Asn	Tyr	Ser	Lys 325	Gly	Gly	Gly	Glu	Asp 330	His	Leu	Gln	Gly 335	Gly	Ala
Leu	Leu	Tyr	Val 340	Asn	Asp	Ser	Arg	Thr 345	Pro	Trp	Ala	Asn	Ser 350	Asp	Tyr
Arg	Arg	Leu 355	Asn	Arg	Thr	Ala	Thr 360	Asn	Gln	Thr	Gly	Thr 365	Ile	Asp	Lys
Ser	Ile 370	Leu	Asp	Glu	Gln	Ser 375	Asp	Pro	Asn	His	Met	Gly 380	Gly	Phe	Asp
Phe 385	Leu	Leu	Ala	Asn	Asp 390	Val	Asp	Leu	Ser	Asn 395	Pro	Val	Val	Gln	Ala 400
Glu	Gln	Leu	Asn	Gln 405	Ile	His	Tyr	Leu	Met	Asn 410	Trp	Gly	Ser	Ile 415	Val
Met	Gly	Asp	Lys 420	Asp	Ala	Asn	Phe	Asp 425	Gly	Ile	Arg	Val	Asp 430	Ala	Val
Asp	Asn	Val 435	Asp	Ala	Asp	Met	Leu	Gln 440	Leu	Tyr	Thr	Asn 445	Tyr	Phe	Arg
Glu	Tyr 450	Tyr	Gly	Val	Asn	Lys 455	Ser	Glu	Ala	Asn	Ala 460	Leu	Ala	His	Ile
Ser 465	Val	Leu	Glu	Ala	Trp 470	Ser	Leu	Asn	Asp	Asn 475	His	Tyr	Asn	Asp	Lys 480
Thr	Asp	Gly	Ala	Ala 485	Leu	Ala	Met	Glu	Asn	Lys 490	Gln	Arg	Leu	Ala 495	Leu
Leu	Phe	Ser	Leu	Ala 500	Lys	Pro	Ile	Lys 505	Glu	Arg	Thr	Pro	Ala 510	Val	Ser
Pro	Leu	Tyr 515	Asn	Asn	Thr	Phe	Asn 520	Thr	Thr	Gln	Arg	Asp 525	Glu	Lys	Thr

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Asp	Trp	Ile	Asn	Lys	Asp	Gly	Ser	Lys	Ala	Tyr	Asn	Glu	Asp	Gly	Thr
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Val	Lys	Gln	Ser	Thr	Ile	Gly	Lys	Tyr	Asn	Glu	Lys	Tyr	Gly	Asp	Ala
545					550					555					560
Ser	Gly	Asn	Tyr	Val	Phe	Ile	Arg	Ala	His	Asp	Asn	Asn	Val	Gln	Asp
				565					570					575	
Ile	Ile	Ala	Glu	Ile	Ile	Lys	Lys	Glu	Ile	Asn	Pro	Lys	Ser	Asp	Gly
			580					585					590		
Phe	Thr	Ile	Thr	Asp	Ala	Glu	Met	Lys	Gln	Ala	Phe	Glu	Ile	Tyr	Asn
			595				600					605			
Lys	Asp	Met	Leu	Ser	Ser	Asp	Lys	Lys	Tyr	Thr	Leu	Asn	Asn	Ile	Pro
610						615					620				
Ala	Ala	Tyr	Ala	Val	Met	Leu	Gln	Asn	Met	Glu	Thr	Ile	Thr	Arg	Val
625					630					635					640
Tyr	Tyr	Gly	Asp	Leu	Tyr	Thr	Asp	Asp	Gly	His	Tyr	Met	Glu	Thr	Lys
				645					650					655	
Ser	Pro	Tyr	Tyr	Asp	Thr	Ile	Val	Asn	Leu	Met	Lys	Ser	Arg	Ile	Lys
			660					665					670		
Tyr	Val	Ser	Gly	Gly	Gln	Ala	Gln	Arg	Ser	Tyr	Trp	Leu	Pro	Thr	Asp
			675				680					685			
Gly	Lys	Met	Asp	Asn	Ser	Asp	Val	Glu	Leu	Tyr	Arg	Thr	Asn	Glu	Val
690						695					700				
Tyr	Thr	Ser	Val	Arg	Tyr	Gly	Lys	Asp	Ile	Met	Thr	Ala	Asn	Asp	Thr
705					710					715					720
Glu	Gly	Ser	Lys	Tyr	Ser	Arg	Thr	Ser	Gly	Gln	Val	Thr	Leu	Val	Ala
				725					730					735	
Asn	Asn	Pro	Lys	Leu	Asn	Leu	Asp	Gln	Ser	Ala	Lys	Leu	Asn	Val	Glu
			740					745					750		
Met	Gly	Lys	Ile	His	Ala	Asn	Gln	Lys	Tyr	Arg	Ala	Leu	Ile	Val	Gly
			755				760					765			
Thr	Ala	Asp	Gly	Ile	Lys	Asn	Phe	Thr	Ser	Asp	Ala	Asp	Ala	Ile	Ala
770					775						780				
Ala	Gly	Tyr	Val	Lys	Glu	Thr	Asp	Ser	Asn	Gly	Val	Leu	Thr	Phe	Gly
785					790					795					800
Ala	Asn	Asp	Ile	Lys	Gly	Tyr	Glu	Thr	Phe	Asp	Met	Ser	Gly	Phe	Val
				805					810					815	
Ala	Val	Trp	Val	Pro	Val	Gly	Ala	Ser	Asp	Asn	Gln	Asp	Ile	Arg	Val
			820					825					830		
Ala	Pro	Ser	Thr	Glu	Ala	Lys	Lys	Glu	Gly	Glu	Leu	Thr	Leu	Lys	Ala
			835				840					845			
Thr	Glu	Ala	Tyr	Asp	Ser	Gln	Leu	Ile	Tyr	Glu	Gly	Phe	Ser	Asn	Phe
850						855					860				
Gln	Thr	Ile	Pro	Asp	Gly	Ser	Asp	Pro	Ser	Val	Tyr	Thr	Asn	Arg	Lys
865					870					875					880
Ile	Ala	Glu	Asn	Val	Asp	Leu	Phe	Lys	Ser	Trp	Gly	Val	Thr	Ser	Phe
				885					890					895	
Glu	Met	Ala	Pro	Gln	Phe	Val	Ser	Ala	Asp	Asp	Gly	Thr	Phe	Leu	Asp
			900					905					910		
Ser	Val	Ile	Gln	Asn	Gly	Tyr	Ala	Phe	Ala	Asp	Arg	Tyr	Asp	Leu	Ala
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Pro	Asp	Gln	Ile	Tyr	Gln	Leu	Pro	Gly	Lys	Glu	Val	Val	Thr	Ala	Thr	965	970	975
Arg	Thr	Asp	Gly	Ala	Gly	Arg	Lys	Ile	Ala	Asp	Ala	Ile	Ile	Asp	His	980	985	990
Ser	Leu	Tyr	Val	Ala	Asn	Ser	Lys	Ser	Ser	Gly	Lys	Asp	Tyr	Gln	Ala	995	1000	1005
Lys	Tyr	Gly	Gly	Glu	Phe	Leu	Ala	Glu	Leu	Lys	Ala	Lys	Tyr	Pro		1010	1015	1020
Glu	Met	Phe	Lys	Val	Asn	Met	Ile	Ser	Thr	Gly	Lys	Pro	Ile	Asp		1025	1030	1035
Asp	Ser	Val	Lys	Leu	Lys	Gln	Trp	Lys	Ala	Glu	Tyr	Phe	Asn	Gly		1040	1045	1050
Thr	Asn	Val	Leu	Glu	Arg	Gly	Val	Gly	Tyr	Val	Leu	Ser	Asp	Glu		1055	1060	1065
Ala	Thr	Gly	Lys	Tyr	Phe	Thr	Val	Thr	Lys	Glu	Gly	Asn	Phe	Ile		1070	1075	1080
Pro	Leu	Gln	Leu	Thr	Gly	Lys	Glu	Lys	Val	Ile	Thr	Gly	Phe	Ser		1085	1090	1095
Ser	Asp	Gly	Lys	Gly	Ile	Thr	Tyr	Phe	Gly	Thr	Ser	Gly	Thr	Gln		1100	1105	1110
Ala	Lys	Ser	Ala	Phe	Val	Thr	Phe	Asn	Gly	Asn	Thr	Tyr	Tyr	Phe		1115	1120	1125
Asp	Ala	Arg	Gly	His	Met	Val	Thr	Asn	Ser	Glu	Tyr	Ser	Pro	Asn		1130	1135	1140
Gly	Lys	Asp	Val	Tyr	Arg	Phe	Leu	Pro	Asn	Gly	Ile	Met	Leu	Ser		1145	1150	1155
Asn	Ala	Phe	Tyr	Ile	Asp	Ala	Asn	Gly	Asn	Thr	Tyr	Leu	Tyr	Asn		1160	1165	1170
Ser	Lys	Gly	Gln	Met	Tyr	Lys	Gly	Gly	Tyr	Thr	Lys	Phe	Asp	Val		1175	1180	1185
Ser	Glu	Thr	Asp	Lys	Asp	Gly	Lys	Glu	Ser	Lys	Val	Val	Lys	Phe		1190	1195	1200
Arg	Tyr	Phe	Thr	Asn	Glu	Gly	Val	Met	Ala	Lys	Gly	Val	Thr	Val		1205	1210	1215
Ile	Asp	Gly	Phe	Thr	Gln	Tyr	Phe	Gly	Glu	Asp	Gly	Phe	Gln	Ala		1220	1225	1230
Lys	Asp	Lys	Leu	Val	Thr	Phe	Lys	Gly	Lys	Thr	Tyr	Tyr	Phe	Asp		1235	1240	1245
Ala	His	Thr	Gly	Asn	Gly	Ile	Lys	Asp	Thr	Trp	Arg	Asn	Ile	Asn		1250	1255	1260
Gly	Lys	Trp	Tyr	Tyr	Phe	Asp	Ala	Asn	Gly	Val	Ala	Ala	Thr	Gly		1265	1270	1275
Ala	Gln	Val	Ile	Asn	Gly	Gln	Lys	Leu	Tyr	Phe	Asn	Glu	Asp	Gly		1280	1285	1290
Ser	Gln	Val	Lys	Gly	Gly	Val	Val	Lys	Asn	Ala	Asp	Gly	Thr	Tyr		1295	1300	1305
Ser	Lys	Tyr	Lys	Glu	Gly	Phe	Gly	Glu	Leu	Val	Thr	Asn	Glu	Phe				

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1310	1315	1320
Phe Thr Thr Asp Gly Asn Val Trp Tyr Tyr Ala Gly Ala Asn Gly		
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Lys Thr Val Thr Gly Ala Gln Val Ile Asn Gly Gln His Leu Tyr		
1340	1345	1350
Phe Asn Ala Asp Gly Ser Gln Val Lys Gly Gly Val Val Lys Asn		
1355	1360	1365
Ala Asp Gly Thr Tyr Ser Lys Tyr Asn Ala Ser Thr Gly Glu Arg		
1370	1375	1380
Leu Thr Asn Glu Phe Phe Thr Thr Gly Asp Asn Asn Trp Tyr Tyr		
1385	1390	1395
Ile Gly Ala Asn Gly Lys Ser Val Thr Gly Glu Val Lys Ile Gly		
1400	1405	1410
Asp Asp Thr Tyr Phe Phe Ala Lys Asp Gly Lys Gln Val Lys Gly		
1415	1420	1425
Gln Thr Val Ser Ala Gly Asn Gly Arg Ile Ser Tyr Tyr Tyr Gly		
1430	1435	1440
Asp Ser Gly Lys Arg Ala Val Ser Thr Trp Ile Glu Ile Gln Pro		
1445	1450	1455
Gly Val Tyr Val Tyr Phe Asp Lys Asn Gly Leu Ala Tyr Pro Pro		
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Arg Val Leu Asn		
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<210> SEQ ID NO 9

<211> LENGTH: 4311

<212> TYPE: DNA

<213> ORGANISM: Streptococcus downei

<400> SEQUENCE: 9

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cgtaccccg ctaatcagac gggtagcctg gacagccgct tcacttataa cgcgaaacgac      720
cctttgggcg gttatgagct gctgctggca aatgacgtcg ataacagcaa tccgatcgtg      780
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ctgctgcaaa ttagcagcga ttacctgaaa gcagcctacg gcattgataa gaataacaaa      960
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gtggatcgtg	aagttgatga	ccgcgagggt	gaaacgggtc	cgagctattc	ttttgcacgt	1200
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<210> SEQ ID NO 10

<211> LENGTH: 1436

<212> TYPE: PRT

<213> ORGANISM: Streptococcus downei

<400> SEQUENCE: 10

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Thr Gly Ala Tyr Lys Asp Thr Ser Lys Val Glu Ala Asp Lys Ser Gly
35          40          45
Ser Asp Ile Ser Lys Glu Glu Thr Thr Phe Ala Ala Asn Asn Arg Ala
50          55          60
Tyr Ser Thr Ser Ala Glu Asn Phe Glu Ala Ile Asp Asn Tyr Leu Thr
65          70          75          80
Ala Asp Ser Trp Tyr Arg Pro Lys Ser Ile Leu Lys Asp Gly Lys Thr
85          90          95
Trp Thr Glu Ser Ser Lys Asp Asp Phe Arg Pro Leu Leu Met Ala Trp
100         105         110
Trp Pro Asp Thr Glu Thr Lys Arg Asn Tyr Val Asn Tyr Met Asn Lys
115         120         125
Val Val Gly Ile Asp Lys Thr Tyr Thr Ala Glu Thr Ser Gln Ala Asp
130         135         140
Leu Thr Ala Ala Ala Glu Leu Val Gln Ala Arg Ile Glu Gln Lys Ile
145         150         155         160
Thr Thr Glu Gln Asn Thr Lys Trp Leu Arg Glu Ala Ile Ser Ala Phe
165         170         175

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Asp	His	Leu	Gln	Asn	Gly	Ala	Leu	Lys	Phe	Asp	Asn	Gln	Ser	Asp	Leu	195	200	205
Thr	Pro	Asp	Thr	Gln	Ser	Asn	Tyr	Arg	Leu	Leu	Asn	Arg	Thr	Pro	Thr	210	215	220
Asn	Gln	Thr	Gly	Ser	Leu	Asp	Ser	Arg	Phe	Thr	Tyr	Asn	Ala	Asn	Asp	225	230	235
Pro	Leu	Gly	Gly	Tyr	Glu	Leu	Leu	Leu	Ala	Asn	Asp	Val	Asp	Asn	Ser	245	250	255
Asn	Pro	Ile	Val	Gln	Ala	Glu	Gln	Leu	Asn	Trp	Leu	His	Tyr	Leu	Leu	260	265	270
Asn	Phe	Gly	Thr	Ile	Tyr	Ala	Lys	Asp	Ala	Asp	Ala	Asn	Phe	Asp	Ser	275	280	285
Ile	Arg	Val	Asp	Ala	Val	Asp	Asn	Val	Asp	Ala	Asp	Leu	Leu	Gln	Ile	290	295	300
Ser	Ser	Asp	Tyr	Leu	Lys	Ala	Ala	Tyr	Gly	Ile	Asp	Lys	Asn	Asn	Lys	305	310	315
Asn	Ala	Asn	Asn	His	Val	Ser	Ile	Val	Glu	Ala	Trp	Ser	Asp	Asn	Asp	325	330	335
Thr	Pro	Tyr	Leu	His	Asp	Asp	Gly	Asp	Asn	Leu	Met	Asn	Met	Asp	Asn	340	345	350
Lys	Phe	Arg	Leu	Ser	Met	Leu	Trp	Ser	Leu	Ala	Lys	Pro	Leu	Asp	Lys	355	360	365
Arg	Ser	Gly	Leu	Asn	Pro	Leu	Ile	His	Asn	Ser	Leu	Val	Asp	Arg	Glu	370	375	380
Val	Asp	Asp	Arg	Glu	Val	Glu	Thr	Val	Pro	Ser	Tyr	Ser	Phe	Ala	Arg	385	390	395
Ala	His	Asp	Ser	Glu	Val	Gln	Asp	Leu	Ile	Arg	Asp	Ile	Ile	Lys	Ala	405	410	415
Glu	Ile	Asn	Pro	Asn	Ala	Phe	Gly	Tyr	Ser	Phe	Thr	Gln	Asp	Glu	Ile	420	425	430
Asp	Gln	Ala	Phe	Lys	Ile	Tyr	Asn	Glu	Asp	Leu	Lys	Lys	Thr	Asp	Lys	435	440	445
Lys	Tyr	Thr	His	Tyr	Asn	Val	Pro	Leu	Ser	Tyr	Thr	Leu	Leu	Leu	Thr	450	455	460
Asn	Lys	Gly	Ser	Ile	Pro	Arg	Val	Tyr	Tyr	Gly	Asp	Met	Phe	Thr	Asp	465	470	475
Asp	Gly	Gln	Tyr	Met	Ala	Asn	Lys	Thr	Val	Asn	Tyr	Asp	Ala	Ile	Glu	485	490	495
Ser	Leu	Leu	Lys	Ala	Arg	Met	Lys	Tyr	Val	Ala	Gly	Gly	Gln	Ala	Met	500	505	510
Gln	Asn	Tyr	Gln	Ile	Gly	Asn	Gly	Glu	Ile	Leu	Thr	Ser	Val	Arg	Tyr	515	520	525
Gly	Lys	Gly	Ala	Leu	Lys	Gln	Ser	Asp	Lys	Gly	Asp	Ala	Thr	Thr	Arg	530	535	540
Thr	Ser	Gly	Val	Gly	Val	Met	Gly	Asn	Gln	Pro	Asn	Phe	Ser	Leu		545	550	555
Asp	Gly	Lys	Val	Val	Ala	Leu	Asn	Met	Gly	Ala	Ala	His	Ala	Asn	Gln	565	570	575
Glu	Tyr	Arg	Ala	Leu	Met	Val	Ser	Thr	Lys	Asp	Gly	Val	Ala	Thr	Tyr			

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580							585					590				
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Asn	Pro	Gln	Val	Ser	Gly	Phe	Leu	Gln	Val	Trp	Val	Pro	Val	Gly	Ala	
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Ala	Asp	Asp	Gln	Asp	Ile	Arg	Val	Ala	Ala	Ser	Asp	Thr	Ala	Ser	Thr	
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Phe	Glu	Gly	Phe	Ser	Asn	Phe	Gln	Ser	Phe	Ala	Thr	Lys	Glu	Glu	Glu	
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Tyr	Thr	Asn	Val	Val	Ile	Ala	Asn	Asn	Val	Asp	Lys	Phe	Val	Ser	Trp	
	690					695					700					
Gly	Ile	Thr	Asp	Phe	Glu	Met	Ala	Pro	Gln	Tyr	Val	Ser	Ser	Thr	Asp	
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Gly	Gln	Phe	Leu	Asp	Ser	Val	Ile	Gln	Asn	Gly	Tyr	Ala	Phe	Thr	Asp	
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Arg	Tyr	Asp	Leu	Gly	Met	Ser	Lys	Ala	Asn	Lys	Tyr	Gly	Thr	Ala	Asp	
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Gln	Leu	Val	Lys	Ala	Ile	Lys	Ala	Leu	His	Ala	Lys	Gly	Leu	Lys	Val	
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Met	Ala	Asp	Trp	Val	Pro	Asp	Gln	Met	Tyr	Thr	Phe	Pro	Lys	Gln	Glu	
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Val	Val	Thr	Val	Thr	Arg	Thr	Asp	Lys	Phe	Gly	Lys	Pro	Ile	Ala	Gly	
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Ser	Gln	Ile	Asn	His	Ser	Leu	Tyr	Val	Thr	Asp	Thr	Lys	Ser	Ser	Gly	
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Glu	Lys	Tyr	Pro	Glu	Leu	Phe	Thr	Lys	Lys	Gln	Ile	Ser	Thr	Gly	Gln	
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Ala	Ile	Asp	Pro	Ser	Val	Lys	Ile	Lys	Gln	Trp	Ser	Ala	Lys	Tyr	Phe	
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Asn	Gly	Ser	Asn	Ile	Leu	Gly	Arg	Gly	Ala	Asp	Tyr	Val	Leu	Ser	Asp	
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Gln	Ala	Ser	Asn	Lys	Tyr	Leu	Asn	Val	Ser	Asp	Asp	Lys	Leu	Phe	Leu	
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Pro	Lys	Thr	Leu	Leu	Gly	Gln	Val	Val	Glu	Ser	Gly	Ile	Arg	Phe	Asp	
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Gly	Tyr	Met	Val	Thr	Gly	Ala	Gln	Asn	Ile	Lys	Gly	Ser	Asn	Tyr	Tyr	
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Phe	Leu	Ala	Asn	Gly	Ala	Ala	Leu	Arg	Asn	Thr	Val	Tyr	Thr	Asp	Ala	
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Val	Met	Ala	Leu	Gly	Leu	Thr	Thr	Val	Asp	Gly	His	Val	Gln	Tyr	
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Phe	Asp	Lys	Asp	Gly	Val	Gln	Ala	Lys	Asp	Lys	Ile	Ile	Val	Thr	
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Asp	Phe	Val	Thr	Ala	Lys	Asp	Gly	Lys	Leu	Tyr	Phe	Tyr	Asp	Val	
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Arg	Val	Tyr	Phe	Lys	Asp	Asn	Gly	His	Gln	Val	Lys	Gly	Gln	Leu	
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Val	Thr	Gly	Asn	Asp	Gly	Lys	Leu	Arg	Tyr	Tyr	Asp	Ala	Asn	Ser	
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Gly	Asp	Gln	Ala	Phe	Asn	Lys	Ser	Val	Thr	Val	Asn	Gly	Lys	Thr	
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Lys	Gly	Gln	Thr	Phe	Lys	Asp	Gly	Ser	Gly	Val	Leu	Arg	Phe	Tyr	
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Asn	Leu	Glu	Gly	Gln	Tyr	Val	Ser	Gly	Ser	Gly	Trp	Tyr	Lys	Asn	
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Ala	Gln	Gly	Gln	Trp	Leu	Tyr	Val	Lys	Asp	Gly	Lys	Val	Leu	Thr	
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Gly	Leu	Gln	Thr	Val	Gly	Asn	Gln	Lys	Val	Tyr	Phe	Asp	Lys	Asn
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Val	Arg	Tyr	Phe	Asp	Glu	Asn	Ser	Gly	Ser	Met	Ile	Thr	Asn	Gln
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Trp	Lys	Phe	Val	Tyr	Gly	Gln	Tyr	Tyr	Tyr	Phe	Gly	Ser	Asp	Gly
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Ala	Ala	Val	Tyr	Arg	Gly	Trp	Asn
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<210> SEQ ID NO 11

<211> LENGTH: 3942

<212> TYPE: DNA

<213> ORGANISM: Streptococcus mutans

<400> SEQUENCE: 11

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3942

<210> SEQ ID NO 12

<211> LENGTH: 1313

<212> TYPE: PRT

<213> ORGANISM: Streptococcus mutans

<400> SEQUENCE: 12

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Thr Asn Phe Thr Leu Ile Ala Asp Gly Lys Ile Leu His Phe Asp Glu
20     25     30

Thr Gly Ala Tyr Thr Asp Thr Ser Ile Asp Thr Val Asn Lys Asp Ile
35     40     45

Val Thr Thr Arg Ser Asn Leu Tyr Lys Lys Tyr Asn Gln Val Tyr Asp
50     55     60

Arg Ser Ala Gln Ser Phe Glu His Val Asp His Tyr Leu Thr Ala Glu
65     70     75     80

Ser Trp Tyr Arg Pro Lys Tyr Ile Leu Lys Asp Gly Lys Thr Trp Thr
85     90     95

Gln Ser Thr Glu Lys Asp Phe Arg Pro Leu Leu Met Thr Trp Trp Pro
100    105    110

Ser Gln Glu Thr Gln Arg Gln Tyr Val Asn Phe Met Asn Ala Gln Leu
115    120    125

Gly Ile Asn Lys Thr Tyr Asp Asp Thr Ser Asn Gln Leu Gln Leu Asn
130    135    140

Ile Ala Ala Ala Thr Ile Gln Ala Lys Ile Glu Ala Lys Ile Thr Thr
145    150    155    160

Leu Lys Asn Thr Asp Trp Leu Arg Gln Thr Ile Ser Ala Phe Val Lys
165    170    175

Thr Gln Ser Ala Trp Asn Ser Asp Ser Glu Lys Pro Phe Asp Asp His
180    185    190

Leu Gln Asn Gly Ala Val Leu Tyr Asp Asn Glu Gly Lys Leu Thr Pro
195    200    205

Tyr Ala Asn Ser Asn Tyr Arg Ile Leu Asn Arg Thr Pro Thr Asn Gln
210    215    220

Thr Gly Lys Lys Asp Pro Arg Tyr Thr Ala Asp Asn Thr Ile Gly Gly
225    230    235    240

Tyr Glu Phe Leu Leu Ala Asn Asp Val Asp Asn Ser Asn Pro Val Val
245    250    255

Gln Ala Glu Gln Leu Asn Trp Leu His Phe Leu Met Asn Phe Gly Asn
260    265    270

Ile Tyr Ala Asn Asp Pro Asp Ala Asn Phe Asp Ser Ile Arg Val Asp
275    280    285

Ala Val Asp Asn Val Asp Ala Asp Leu Leu Gln Ile Ala Gly Asp Tyr
290    295    300

Leu Lys Ala Ala Lys Gly Ile His Lys Asn Asp Lys Ala Ala Asn Asp
305    310    315    320

His Leu Ser Ile Leu Glu Ala Trp Ser Asp Asn Asp Thr Pro Tyr Leu
325    330    335

His Asp Asp Gly Asp Asn Met Ile Asn Met Asp Asn Lys Leu Arg Leu
340    345    350

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Asn	Pro	Leu	Ile	Thr	Asn	Ser	Leu	Val	Asn	Arg	Thr	Asp	Asp	Asn	Ala
	370					375					380				
Glu	Thr	Ala	Ala	Val	Pro	Ser	Tyr	Ser	Phe	Ile	Arg	Ala	His	Asp	Ser
385					390					395					400
Glu	Val	Gln	Asp	Leu	Ile	Arg	Asp	Ile	Ile	Lys	Ala	Glu	Ile	Asn	Pro
			405					410						415	
Asn	Val	Val	Gly	Tyr	Ser	Phe	Thr	Met	Glu	Glu	Ile	Lys	Lys	Ala	Phe
			420					425						430	
Glu	Ile	Tyr	Asn	Lys	Asp	Leu	Leu	Ala	Thr	Glu	Lys	Lys	Tyr	Thr	His
	435					440						445			
Tyr	Asn	Thr	Ala	Leu	Ser	Tyr	Ala	Leu	Leu	Leu	Thr	Asn	Lys	Ser	Ser
	450					455					460				
Val	Pro	Arg	Val	Tyr	Tyr	Gly	Asp	Met	Phe	Thr	Asp	Asp	Gly	Gln	Tyr
465					470					475					480
Met	Ala	His	Lys	Thr	Ile	Asn	Tyr	Glu	Ala	Ile	Glu	Thr	Leu	Leu	Lys
			485					490						495	
Ala	Arg	Ile	Lys	Tyr	Val	Ser	Gly	Gly	Gln	Ala	Met	Arg	Asn	Gln	Gln
			500					505					510		
Val	Gly	Asn	Ser	Glu	Ile	Ile	Thr	Ser	Val	Arg	Tyr	Gly	Lys	Gly	Ala
	515						520					525			
Leu	Lys	Ala	Met	Asp	Thr	Gly	Asp	Arg	Thr	Thr	Arg	Thr	Ser	Gly	Val
	530					535					540				
Ala	Val	Ile	Glu	Gly	Asn	Asn	Pro	Ser	Leu	Arg	Leu	Lys	Ala	Ser	Asp
545					550					555					560
Arg	Val	Val	Val	Asn	Met	Gly	Ala	Ala	His	Lys	Asn	Gln	Ala	Tyr	Arg
				565					570					575	
Pro	Leu	Leu	Leu	Thr	Thr	Asp	Asn	Gly	Ile	Lys	Ala	Tyr	His	Ser	Asp
		580					585						590		
Gln	Glu	Ala	Ala	Gly	Leu	Val	Arg	Tyr	Thr	Asn	Asp	Arg	Gly	Glu	Leu
	595					600						605			
Ile	Phe	Thr	Ala	Ala	Asp	Ile	Lys	Gly	Tyr	Ala	Asn	Pro	Gln	Val	Ser
610					615						620				
Gly	Tyr	Leu	Gly	Val	Trp	Val	Pro	Val	Gly	Ala	Ala	Ala	Asp	Gln	Asp
625					630					635				640	
Val	Arg	Val	Ala	Ala	Ser	Thr	Ala	Pro	Ser	Thr	Asp	Gly	Lys	Ser	Val
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His	Gln	Asn	Ala	Ala	Leu	Asp	Ser	Arg	Val	Met	Phe	Glu	Gly	Phe	Ser
		660						665					670		
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Ile	Ala	Lys	Asn	Val	Asp	Lys	Phe	Ala	Glu	Trp	Gly	Val	Thr	Asp	Phe
	690					695					700				
Glu	Met	Ala	Pro	Gln	Tyr	Val	Ser	Ser	Thr	Asp	Gly	Ser	Phe	Leu	Asp
705					710					715					720
Ser	Val	Ile	Gln	Asn	Gly	Tyr	Ala	Phe	Thr	Asp	Arg	Tyr	Asp	Leu	Gly
			725					730						735	
Ile	Ser	Lys	Pro	Asn	Lys	Tyr	Gly	Thr	Ala	Asp	Asp	Leu	Val	Lys	Ala
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Ile	Lys	Ala	Leu	His	Ser	Lys	Gly	Ile	Lys	Val	Met	Ala	Asp	Trp	Val	
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Pro	Asp	Gln	Met	Tyr	Ala	Leu	Pro	Glu	Lys	Glu	Val	Val	Thr	Ala	Thr	
	770					775					780					
Arg	Val	Asp	Lys	Tyr	Gly	Thr	Pro	Val	Ala	Gly	Ser	Gln	Ile	Lys	Asn	
	785				790					795					800	
Thr	Leu	Tyr	Val	Val	Asp	Gly	Lys	Ser	Ser	Gly	Lys	Asp	Gln	Gln	Ala	
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Lys	Tyr	Gly	Gly	Ala	Phe	Leu	Glu	Glu	Leu	Gln	Ala	Lys	Tyr	Pro	Glu	
			820					825					830			
Leu	Phe	Ala	Arg	Lys	Gln	Ile	Ser	Thr	Gly	Val	Pro	Met	Asp	Pro	Ser	
		835					840					845				
Val	Lys	Ile	Lys	Gln	Trp	Ser	Ala	Lys	Tyr	Phe	Asn	Gly	Thr	Asn	Ile	
	850					855					860					
Leu	Gly	Arg	Gly	Ala	Gly	Tyr	Val	Leu	Lys	Asp	Gln	Ala	Thr	Asn	Thr	
	865				870					875					880	
Tyr	Phe	Asn	Ile	Ser	Asp	Asn	Lys	Glu	Ile	Asn	Phe	Leu	Pro	Lys	Thr	
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Leu	Leu	Asn	Gln	Asp	Ser	Gln	Val	Gly	Phe	Ser	Tyr	Asp	Gly	Lys	Gly	
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Tyr	Val	Tyr	Tyr	Ser	Thr	Ser	Gly	Tyr	Gln	Ala	Lys	Asn	Thr	Phe	Ile	
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Ser	Glu	Gly	Asp	Lys	Trp	Tyr	Tyr	Phe	Asp	Asn	Asn	Gly	Tyr	Met	Val	
	930					935					940					
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Gly	Leu	Gln	Leu	Arg	Asp	Ala	Ile	Leu	Lys	Asn	Glu	Asp	Gly	Thr	Tyr	
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Gly	Leu	Thr	Val	Ile	Asp	Gly	Gln	Val	Gln	Tyr	Phe	Asp	Glu	Met		
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Gly	Ala	Ala	Val	Thr	Gly	Ser	Gln	Thr	Ile	Asn	Gly	Gln	His	Leu		
	1070					1075						1080				
Tyr	Phe	Arg	Ala	Asn	Gly	Val	Gln	Val	Lys	Gly	Glu	Phe	Val	Thr		
	1085					1090						1095				
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Tyr	Phe	Asp	Asn	Asn	Gly	Tyr	Ala	Val	Thr	Gly	Ala	Arg	Thr	Ile		
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Gln Gly Gln Trp Phe Tyr Phe Asp Asn Asn Gly Tyr Ala Val Thr		
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Gly Ala Arg Thr Ile Asn Gly Gln His Leu Tyr Phe Arg Ala Asn		
1205	1210	1215
Gly Val Gln Val Lys Gly Glu Phe Val Thr Asp Arg Tyr Gly Arg		
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1235	1240	1245
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1250	1255	1260
Gly Tyr Ala Val Thr Gly Ala Arg Thr Ile Asn Gly Gln His Leu		
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Tyr Phe Arg Ala Asn Gly Val Gln Val Lys Gly Glu Phe Val Thr		
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<210> SEQ ID NO 13

<211> LENGTH: 3972

<212> TYPE: DNA

<213> ORGANISM: Streptococcus dentirousetti

<400> SEQUENCE: 13

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<210> SEQ ID NO 14

<211> LENGTH: 1323

<212> TYPE: PRT

<213> ORGANISM: Streptococcus dentirousetti

<400> SEQUENCE: 14

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Thr Gly Ala Tyr Lys Asp Thr Ser Lys Val Asp Ala Asp Lys Thr Ser
35           40           45

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Ser Ser Val Asn Gln Thr Thr Glu Thr Phe Ala Ala Asn Asn Arg Ala
50           55           60

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Tyr Ser Thr Ala Ala Glu Asn Phe Glu Ala Ile Asp Asn Tyr Leu Thr
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Ala Asp Ser Trp Tyr Arg Pro Lys Ser Ile Leu Lys Asp Gly Thr Thr
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Trp Thr Glu Ser Thr Lys Asp Asp Phe Arg Pro Leu Leu Met Ala Trp
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Trp Pro Asp Thr Glu Thr Lys Arg Asn Tyr Val Asn Tyr Met Asn Lys
115          120          125

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Val Val Gly Ile Asp Lys Thr Tyr Thr Ala Glu Thr Ser Gln Ala Asp
130          135          140

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Leu Thr Ala Ala Ala Glu Leu Val Gln Ala Arg Ile Glu Gln Lys Ile
145          150          155          160

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Thr Ser Glu Lys Asn Thr Lys Trp Leu Arg Glu Ala Ile Ser Ala Phe
165          170          175

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Val Lys Thr Gln Pro Gln Trp Asn Gly Glu Ser Glu Lys Pro Tyr Asp
180          185          190

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Asp His Leu Gln Asn Gly Ala Leu Lys Phe Asp Asn Glu Thr Ser Leu
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Thr Pro Asp Thr Gln Ser Gly Tyr Arg Ile Leu Asn Arg Thr Pro Thr
210          215          220

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Asn Gln Thr Gly Ser Leu Asp Pro Arg Phe Thr Phe Asn Gln Asn Asp

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Thr	Pro	Tyr	Leu	Asn	Asp	Asp	Gly	Asp	Asn	Leu	Met	Asn	Met	Asp	Asn									
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Arg	Ser	Gly	Leu	Asn	Pro	Leu	Ile	His	Asn	Ser	Val	Val	Asp	Arg	Glu									
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Ala	His	Asp	Ser	Glu	Val	Gln	Asp	Leu	Ile	Arg	Asp	Ile	Ile	Lys	Ala									
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Glu	Ile	Asn	Pro	Asn	Ser	Phe	Gly	Tyr	Ser	Phe	Thr	Gln	Glu	Glu	Ile									
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Asp	Gln	Ala	Phe	Lys	Ile	Tyr	Asn	Glu	Asp	Leu	Lys	Lys	Thr	Asn	Lys									
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Lys	Tyr	Thr	His	Tyr	Asn	Val	Pro	Leu	Ser	Tyr	Thr	Leu	Leu	Leu	Thr									
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Asn	Lys	Gly	Ser	Ile	Pro	Arg	Ile	Tyr	Tyr	Gly	Asp	Met	Phe	Thr	Asp									
465					470					475									480					
Asp	Gly	Gln	Tyr	Met	Ala	Asn	Lys	Thr	Val	Asn	Tyr	Asp	Ala	Ile	Glu									
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Ser	Leu	Leu	Lys	Ala	Arg	Met	Lys	Tyr	Val	Ser	Gly	Gly	Gln	Ala	Met									
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Tyr	Thr	Asn	Val	Val	Ile	Ala	Lys	Asn	Val	Asp	Lys	Phe	Val	Ser
690						695				700				
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Gln	Leu	Val	Ala	Ala	Ile	Lys	Ala	Leu	His	Ala	Lys	Gly	Leu	Arg
755						760						765		Val
Met	Ala	Asp	Trp	Val	Pro	Asp	Gln	Met	Tyr	Thr	Phe	Pro	Lys	Lys
770						775				780		Glu		
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785				790						795		800		
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Glu	Lys	Tyr	Pro	Glu	Leu	Phe	Thr	Lys	Lys	Gln	Ile	Ser	Thr	Gly
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Ala	Ile	Asp	Pro	Ser	Val	Lys	Ile	Lys	Gln	Trp	Ser	Ala	Lys	Tyr
850						855				860		Phe		
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865				870						875		880		
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		885						890				895		Leu
Pro	Ala	Ala	Met	Leu	Gly	Lys	Val	Val	Glu	Ser	Gly	Ile	Arg	Phe
		900						905				910		Asp
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915						920						925		Lys
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Asp	Gly	Lys	Ser	His	Tyr	Tyr	Ala	Asn	Asp	Gly	Lys	Arg	Tyr	Glu
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Gly	Tyr	Tyr	Gln	Phe	Gly	Asn	Asp	Ser	Trp	Arg	Tyr	Phe	Glu	Asn
995						1000						1005		Gly
Val	Met	Ala	Val	Gly	Leu	Thr	Arg	Val	Ala	Gly	His	Asp	Gln	Tyr
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Phe	Asp	Lys	Asp	Gly	Ile	Gln	Ala	Lys	Asn	Lys	Ile	Ile	Val	Thr
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1070						1075					1080			
Lys	Gln	His	Leu	Tyr	Phe	Glu	Ala	Asn	Gly	Gln	Gln	Val	Lys	Gly
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<210> SEQ ID NO 15

<211> LENGTH: 4047

<212> TYPE: DNA

<213> ORGANISM: Streptococcus oralis

<400> SEQUENCE: 15

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<210> SEQ ID NO 16

<211> LENGTH: 1348

<212> TYPE: PRT

<213> ORGANISM: Streptococcus oralis

<400> SEQUENCE: 16

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Glu Thr Gly Ala Leu Val Asp Ser Asn Glu Tyr Gln Phe Gln Gln Gly
35          40          45

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Thr Ser Ser Leu Asn Asn Glu Phe Ser Gln Lys Asn Ala Phe Tyr Gly
50          55          60

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Thr Thr Asp Lys Asp Ile Glu Thr Val Asp Gly Tyr Leu Thr Ala Asp
65          70          75          80

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Ser Trp Tyr Arg Pro Lys Phe Ile Leu Lys Asp Gly Lys Thr Trp Thr
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Ala Ser Thr Glu Thr Asp Leu Arg Pro Leu Leu Met Ala Trp Trp Pro

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Val	Gln	Ala	Glu	Gln	Leu	Asn	Trp	Leu	His	Tyr	Met	Met	Asn	Phe	Gly		
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Ser	Ile	Val	Ala	Asn	Asp	Pro	Thr	Ala	Asn	Phe	Asp	Gly	Val	Arg	Val		
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Asp	Ala	Val	Asp	Asn	Val	Asn	Ala	Asp	Leu	Leu	Gln	Ile	Ala	Ser	Asp		
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Tyr	Phe	Lys	Ser	Arg	Tyr	Lys	Val	Gly	Glu	Ser	Glu	Glu	Glu	Ala	Ile		
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Lys	His	Leu	Ser	Ile	Leu	Glu	Ala	Trp	Ser	Asp	Asn	Asp	Pro	Asp	Tyr		
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Asn	Lys	Asp	Thr	Lys	Gly	Ala	Gln	Leu	Ala	Ile	Asp	Asn	Lys	Leu	Arg		
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Leu	Ser	Leu	Leu	Tyr	Ser	Phe	Met	Arg	Asn	Leu	Ser	Ile	Arg	Ser	Gly		
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Val	Glu	Pro	Thr	Ile	Thr	Asn	Ser	Leu	Asn	Asp	Arg	Ser	Ser	Glu	Lys		
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Pro	Asn	Thr	Asp	Gly	Leu	Thr	Phe	Thr	Met	Asp	Glu	Leu	Lys	Gln	Ala		
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Phe	Lys	Ile	Tyr	Asn	Glu	Asp	Met	Arg	Lys	Ala	Asp	Lys	Lys	Tyr	Thr		
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Gln	Phe	Asn	Ile	Pro	Thr	Ala	His	Ala	Leu	Met	Leu	Ser	Asn	Lys	Asp		
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Ser	Ile	Thr	Arg	Val	Tyr	Tyr	Gly	Asp	Leu	Tyr	Thr	Asp	Asp	Gly	Gln		
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Tyr	Met	Glu	Lys	Lys	Ser	Pro	Tyr	His	Asp	Ala	Ile	Asp	Ala	Leu	Leu		
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Arg	Ala	Arg	Ile	Lys	Tyr	Val	Ala	Gly	Gly	Gln	Asp	Met	Lys	Val	Thr		
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Asn	Pro	Asn	Leu	Lys	Leu	Asn	Glu	Trp	Asp	Lys	Leu	Gln	Val	Asn	Met
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Leu	Trp	Lys	Lys	Thr	Asp	Ala	Asn	Gly	Ile	Leu	Thr	Phe	Asp	Met	Asn
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Tyr	Val	Ser	Ser	Gln	Asp	Gly	Thr	Phe	Leu	Asp	Ser	Ile	Ile	Gln	Asn
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Tyr	Tyr	Val	Leu	Lys	Asp	Trp	Ala	Ser	Asn	Asp	Tyr	Leu	Thr	Asn	Arg
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Tyr	Tyr	Phe	Asp	Lys	Arg	Gly	Tyr	Leu	Val	Thr	Gly	Ala	His	Glu	Ile
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Asp	Gly	Lys	His	Val	Tyr	Phe	Leu	Lys	Asn	Gly	Ile	Gln	Leu	Arg	Asp
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Ser	Ile	Arg	Glu	Asp	Glu	Asn	Gly	Asn	Gln	Tyr	Tyr	Tyr	Asp	Gln	Thr
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<212> TYPE: DNA		
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4047

<210> SEQ ID NO 18

<211> LENGTH: 1348

<212> TYPE: PRT

<213> ORGANISM: Streptococcus sanguinis

<400> SEQUENCE: 18

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Glu Thr Gly Ala Leu Ile Asp Ser Ala Glu Tyr Gln Phe Gln Gln Gly
35           40           45

Thr Ser Ser Leu Asn Asn Glu Phe Thr Gln Lys Asn Ala Phe Tyr Gly
50           55           60

Thr Thr Asp Lys Asp Val Glu Thr Ile Asp Gly Tyr Leu Thr Ala Asp
65           70           75           80

Ser Trp Tyr Arg Pro Lys Phe Ile Leu Lys Asp Gly Lys Thr Trp Thr
85           90           95

Ala Ser Thr Glu Ile Asp Leu Arg Pro Leu Leu Met Ala Trp Trp Pro
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Leu Gly Ala Gly Ala Phe Glu Asn Lys Val Glu Gln Ala Ile Leu Thr
130          135          140

Gly Ala Ser Gln Gln Val Gln Arg Lys Ile Glu Glu Arg Ile Gly Lys
145          150          155          160

Glu Gly Asp Thr Lys Trp Leu Arg Thr Leu Met Gly Ala Phe Val Lys
165          170          175

Thr Gln Pro Asn Trp Asn Ile Lys Thr Glu Ser Glu Thr Thr Gly Thr
180          185          190

Asn Lys Asp His Leu Gln Gly Gly Ala Leu Leu Tyr Ser Asn Ser Asp
195          200          205

Lys Thr Ser His Ala Asn Ser Lys Tyr Arg Ile Leu Asn Arg Thr Pro
210          215          220

Thr Asn Gln Thr Gly Thr Pro Lys Tyr Phe Ile Asp Lys Ser Asn Gly
225          230          235          240

Gly Tyr Glu Phe Leu Leu Ala Asn Asp Phe Asp Asn Ser Asn Pro Ala
245          250          255

Val Gln Ala Glu Gln Leu Asn Trp Leu His Phe Met Met Asn Phe Gly
260          265          270

Ser Ile Val Ala Asn Asp Pro Thr Ala Asn Phe Asp Gly Val Arg Val
275          280          285

Asp Ala Val Asp Asn Val Asn Ala Asp Leu Leu Gln Ile Ala Ser Asp
290          295          300

Tyr Phe Lys Ser Arg Tyr Lys Val Gly Glu Ser Glu Glu Glu Ala Ile
305          310          315          320

Lys His Leu Ser Ile Leu Glu Ala Trp Ser Asp Asn Asp Pro Asp Tyr
325          330          335

Asn Lys Asp Thr Lys Gly Ala Gln Leu Pro Ile Asp Asn Lys Leu Arg
340          345          350

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Leu	Ser	Leu	Tyr	Ser	Phe	Met	Arg	Lys	Leu	Ser	Ile	Arg	Ser	Gly	
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Val	Glu	Pro	Thr	Ile	Thr	Asn	Ser	Leu	Asn	Asp	Arg	Ser	Thr	Glu	Lys
370						375			380						
Lys	Asn	Gly	Glu	Arg	Met	Ala	Asn	Tyr	Ile	Phe	Val	Arg	Ala	His	Asp
385						390			395					400	
Ser	Glu	Val	Gln	Thr	Val	Ile	Ala	Asp	Ile	Ile	Arg	Glu	Asn	Ile	Asn
405						410			415						
Pro	Asn	Thr	Asp	Gly	Leu	Thr	Phe	Thr	Met	Asp	Glu	Leu	Lys	Gln	Ala
420						425			430						
Phe	Lys	Ile	Tyr	Asn	Glu	Asp	Met	Arg	Lys	Ala	Asp	Lys	Lys	Tyr	Thr
435						440			445						
Gln	Phe	Asn	Ile	Pro	Thr	Ala	His	Ala	Leu	Met	Leu	Ser	Asn	Lys	Asp
450						455			460						
Ser	Ile	Thr	Arg	Val	Tyr	Tyr	Gly	Asp	Leu	Tyr	Thr	Asp	Asp	Gly	Gln
465						470			475					480	
Tyr	Met	Glu	Lys	Lys	Ser	Pro	Tyr	His	Asp	Ala	Ile	Asp	Ala	Leu	Leu
485						490			495						
Arg	Ala	Arg	Ile	Lys	Tyr	Val	Ala	Gly	Gly	Gln	Asp	Met	Lys	Val	Thr
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Tyr	Met	Gly	Val	Pro	Arg	Glu	Ala	Asp	Lys	Trp	Ser	Tyr	Asn	Gly	Ile
515						520			525						
Leu	Thr	Ser	Val	Arg	Tyr	Gly	Thr	Gly	Ala	Asn	Glu	Ala	Thr	Asp	Glu
530						535			540						
Gly	Thr	Ala	Glu	Thr	Arg	Thr	Gln	Gly	Met	Ala	Val	Ile	Ala	Ser	Asn
545						550			555					560	
Asn	Pro	Asn	Leu	Lys	Leu	Asn	Glu	Trp	Asp	Lys	Leu	Gln	Val	Asn	Met
565						570			575						
Gly	Ala	Ala	His	Lys	Asn	Gln	Tyr	Tyr	Arg	Pro	Val	Leu	Leu	Thr	Thr
580						585			590						
Lys	Asp	Gly	Ile	Ser	Arg	Tyr	Leu	Thr	Asp	Glu	Glu	Val	Pro	Gln	Ser
595						600			605						
Leu	Trp	Lys	Lys	Thr	Asp	Ala	Asn	Gly	Ile	Leu	Thr	Phe	Asp	Met	Asn
610						615			620						
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625						630			635					640	
Trp	Val	Pro	Val	Gly	Ala	Lys	Ala	Asp	Gln	Asp	Ala	Arg	Val	Thr	Ala
645						650			655						
Ser	Lys	Lys	Lys	Asn	Ala	Ser	Gly	Gln	Val	Tyr	Glu	Ser	Ser	Ala	Ala
660						665			670						
Leu	Asp	Ser	Gln	Leu	Ile	Tyr	Glu	Gly	Phe	Ser	Asn	Phe	Gln	Asp	Phe
675						680			685						
Ala	Thr	Arg	Asp	Asp	Gln	Tyr	Thr	Asn	Lys	Val	Ile	Ala	Lys	Asn	Val
690						695			700						
Asn	Leu	Phe	Lys	Glu	Trp	Gly	Val	Thr	Ser	Phe	Glu	Leu	Pro	Pro	Gln
705						710			715					720	
Tyr	Val	Ser	Ser	Gln	Asp	Gly	Thr	Phe	Leu	Asp	Ser	Ile	Ile	Gln	Asn
725						730			735						
Gly	Tyr	Ala	Phe	Glu	Asp	Arg	Tyr	Asp	Met	Ala	Met	Ser	Lys	Asn	Asn
740						745			750						

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Lys	Tyr	Gly	Ser	Leu	Asn	Asp	Leu	Leu	Asn	Ala	Leu	Arg	Ala	Leu	His
		755					760					765			
Ser	Val	Asn	Ile	Gln	Ala	Ile	Ala	Asp	Trp	Val	Pro	Asp	Gln	Ile	Tyr
	770					775					780				
Asn	Leu	Pro	Gly	Lys	Glu	Val	Val	Thr	Ala	Thr	Arg	Val	Asn	Asn	Tyr
	785				790					795					800
Gly	Thr	Tyr	Arg	Glu	Gly	Ser	Glu	Ile	Lys	Glu	Asn	Leu	Tyr	Val	Ala
			805						810					815	
Asn	Thr	Lys	Thr	Asn	Gly	Thr	Asp	Tyr	Gln	Gly	Lys	Tyr	Gly	Gly	Ala
			820					825					830		
Phe	Leu	Asp	Glu	Leu	Lys	Ala	Lys	Tyr	Pro	Glu	Ile	Phe	Glu	Arg	Val
		835					840					845			
Gln	Ile	Ser	Asn	Gly	Gln	Lys	Met	Thr	Thr	Asp	Glu	Lys	Ile	Thr	Lys
	850					855					860				
Trp	Ser	Ala	Lys	His	Phe	Asn	Gly	Thr	Asn	Ile	Leu	Gly	Arg	Gly	Ala
	865				870					875					880
Tyr	Tyr	Val	Leu	Lys	Asp	Trp	Ala	Ser	Asn	Glu	Tyr	Leu	Asn	Asn	Lys
			885						890					895	
Asn	Gly	Glu	Met	Val	Leu	Pro	Lys	Gln	Leu	Val	Asn	Lys	Asn	Ala	Tyr
			900					905					910		
Thr	Gly	Phe	Val	Ser	Asp	Ala	Ser	Gly	Thr	Lys	Tyr	Tyr	Ser	Thr	Ser
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Gly	Tyr	Gln	Ala	Arg	Asn	Ser	Phe	Ile	Gln	Asp	Glu	Asn	Gly	Asn	Trp
	930				935						940				
Tyr	Tyr	Phe	Asn	Asn	Arg	Gly	Tyr	Leu	Val	Thr	Gly	Ala	Gln	Glu	Ile
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Asp	Gly	Lys	Gln	Leu	Tyr	Phe	Leu	Lys	Asn	Gly	Ile	Gln	Leu	Arg	Asp
			965						970					975	
Ser	Leu	Arg	Glu	Asp	Glu	Asn	Gly	Asn	Gln	Tyr	Tyr	Tyr	Asp	Lys	Thr
		980						985					990		
Gly	Ala	Gln	Val	Leu	Asn	Arg	Tyr	Tyr	Thr	Thr	Asp	Gly	Gln	Asn	Trp
		995					1000					1005			
Arg	Tyr	Phe	Asp	Val	Lys	Gly	Val	Met	Ala	Arg	Gly	Leu	Val	Thr	
	1010					1015					1020				
Met	Gly	Gly	Asn	Gln	Gln	Phe	Phe	Asp	Gln	Asn	Gly	Tyr	Gln	Val	
	1025					1030					1035				
Lys	Gly	Lys	Ile	Ala	Arg	Ala	Lys	Asp	Gly	Lys	Leu	Arg	Tyr	Phe	
	1040					1045					1050				
Asp	Lys	Asp	Ser	Gly	Asn	Ala	Ala	Ala	Asn	Arg	Phe	Ala	Gln	Gly	
	1055					1060					1065				
Asp	Asn	Pro	Ser	Asp	Trp	Tyr	Tyr	Phe	Gly	Ala	Asp	Gly	Val	Ala	
	1070					1075					1080				
Val	Thr	Gly	Leu	Gln	Lys	Val	Gly	Gln	Gln	Thr	Leu	Tyr	Phe	Asp	
	1085					1090					1095				
Gln	Asp	Gly	Lys	Gln	Val	Lys	Gly	Lys	Val	Val	Thr	Leu	Ala	Asp	
	1100					1105					1110				
Lys	Ser	Ile	Arg	Tyr	Phe	Asp	Ala	Asn	Ser	Gly	Glu	Met	Ala	Val	
	1115					1120					1125				
Asn	Lys	Phe	Val	Glu	Gly	Ala	Lys	Asn	Val	Trp	Tyr	Tyr	Phe	Asp	
	1130					1135					1140				
Gln	Ala	Gly	Lys	Ala	Val	Thr	Gly	Leu	Gln	Thr	Ile	Asn	Lys	Gln	

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1145	1150	1155
Val Leu Tyr Phe Asp Gln Asp Gly Lys Gln Val Lys Gly Lys Val		
1160	1165	1170
Val Thr Leu Ala Asp Lys Ser Ile Arg Tyr Phe Asp Ala Asn Ser		
1175	1180	1185
Gly Glu Met Ala Val Gly Lys Phe Ala Glu Gly Ala Lys Asn Glu		
1190	1195	1200
Trp Tyr Tyr Phe Asp Gln Ala Gly Lys Ala Val Thr Gly Leu Gln		
1205	1210	1215
Lys Ile Gly Gln Gln Thr Leu Tyr Phe Asp Gln Asn Gly Lys Gln		
1220	1225	1230
Val Lys Gly Lys Val Val Thr Leu Ala Asp Lys Ser Ile Arg Tyr		
1235	1240	1245
Phe Asp Ala Asn Ser Gly Glu Met Ala Ser Asn Lys Phe Val Glu		
1250	1255	1260
Gly Ala Lys Asn Glu Trp Tyr Tyr Phe Asp Gln Ala Gly Lys Ala		
1265	1270	1275
Val Thr Gly Leu Gln Gln Ile Gly Gln Gln Thr Leu Tyr Phe Asp		
1280	1285	1290
Gln Asn Gly Lys Gln Val Lys Gly Lys Ile Val Tyr Val Asn Gly		
1295	1300	1305
Ala Asn Arg Tyr Phe Asp Ala Asn Ser Gly Glu Met Ala Arg Asn		
1310	1315	1320
Lys Trp Ile Gln Leu Glu Asp Gly Ser Trp Met Tyr Phe Asp Arg		
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<210> SEQ ID NO 19

<211> LENGTH: 4023

<212> TYPE: DNA

<213> ORGANISM: unknown

<220> FEATURE:

<223> OTHER INFORMATION: unknown Streptococcus sp. C150

<400> SEQUENCE: 19

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gcgtatgact ccagcgaggc ctctttcgag ctgattgacg gttatctgac tgcggactct      240
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aacaagaga ctgagaacta cagcaagggc ggtggtgagg accatctgca aggtggtgcc      600
ctgctgtatg ttaatgactc tcgtaccccg tgggcgaaca gcaactatcg tttgctgaac      660
cgcacggcga ccaaccagac cggtacgacg gacaagagca tcctggacga gcagagcgat      720
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gcggacatgc	tgcaattgta	caccaactat	ttccgcgaat	actatggtgt	caacaaaagc	960
gaggcaaacg	cgctggcgca	cattagcgtc	ctggaagcct	ggagcctgaa	tgacaaccat	1020
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gcgttcgtca	cttttaacgg	taaacgtac	tacttcgacg	cacgtggcca	catggttacc	3000
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<210> SEQ ID NO 20
<211> LENGTH: 1340
<212> TYPE: PRT
<213> ORGANISM: unknown
<220> FEATURE:
<223> OTHER INFORMATION: unknown Streptococcus sp. C150

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<400> SEQUENCE: 20

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20            25            30

Asp Gly Ala Leu Thr Ser Ser Ser Thr Tyr Ser Phe Thr Gln Gly Thr
35            40            45

Thr Asn Ile Val Asp Gly Phe Ser Ile Asn Asn Arg Ala Tyr Asp Ser
50            55            60

Ser Glu Ala Ser Phe Glu Leu Ile Asp Gly Tyr Leu Thr Ala Asp Ser
65            70            75            80

Trp Tyr Arg Pro Ala Ser Ile Ile Lys Asp Gly Val Thr Trp Gln Ala
85            90            95

Ser Thr Ala Glu Asp Phe Arg Pro Leu Leu Met Ala Trp Trp Pro Asn
100           105           110

Val Asp Thr Gln Val Asn Tyr Leu Asn Tyr Met Ser Lys Val Phe Asn
115           120           125

Leu Asp Ala Lys Tyr Ser Ser Thr Asp Lys Gln Glu Thr Leu Lys Val
130           135           140

Ala Ala Lys Asp Ile Gln Ile Lys Ile Glu Gln Lys Ile Gln Ala Glu
145           150           155           160

Lys Ser Thr Gln Trp Leu Arg Glu Thr Ile Ser Ala Phe Val Lys Thr

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Glu	Asp	His	Leu	Gln	Gly	Gly	Ala	Leu	Leu	Tyr	Val	Asn	Asp	Ser
	195						200					205		Arg
Thr	Pro	Trp	Ala	Asn	Ser	Asn	Tyr	Arg	Leu	Leu	Asn	Arg	Thr	Ala
	210					215					220			Thr
Asn	Gln	Thr	Gly	Thr	Ile	Asp	Lys	Ser	Ile	Leu	Asp	Glu	Gln	Ser
	225				230					235				240
Pro	Asn	His	Met	Gly	Gly	Phe	Asp	Phe	Leu	Leu	Ala	Asn	Asp	Val
			245						250					255
Leu	Ser	Asn	Pro	Val	Val	Gln	Ala	Glu	Gln	Leu	Asn	Gln	Ile	His
		260						265					270	Tyr
Leu	Met	Asn	Trp	Gly	Ser	Ile	Val	Met	Gly	Asp	Lys	Asp	Ala	Asn
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Asp	Gly	Ile	Arg	Val	Asp	Ala	Val	Asp	Asn	Val	Asp	Ala	Asp	Met
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Gln	Leu	Tyr	Thr	Asn	Tyr	Phe	Arg	Glu	Tyr	Tyr	Gly	Val	Asn	Lys
	305				310						315			320
Glu	Ala	Asn	Ala	Leu	Ala	His	Ile	Ser	Val	Leu	Glu	Ala	Trp	Ser
			325						330					335
Asn	Asp	Asn	His	Tyr	Asn	Asp	Lys	Thr	Asp	Val	Ala	Ala	Leu	Ala
		340						345					350	Met
Glu	Asn	Lys	Gln	Arg	Leu	Ala	Leu	Leu	Phe	Ser	Leu	Ala	Lys	Pro
		355					360					365		Ile
Lys	Glu	Arg	Thr	Pro	Ala	Val	Ser	Pro	Leu	Tyr	Asn	Asn	Thr	Phe
	370					375					380			Asn
Thr	Thr	Gln	Arg	Asp	Glu	Lys	Thr	Asp	Trp	Ile	Asn	Lys	Asp	Gly
	385				390					395				400
Lys	Ala	Tyr	Asn	Glu	Asp	Gly	Thr	Val	Lys	Lys	Ser	Thr	Ile	Gly
			405						410					415
Tyr	Asn	Glu	Lys	Tyr	Gly	Asp	Ala	Ser	Gly	Asn	Tyr	Val	Phe	Ile
		420						425					430	Arg
Ala	His	Asp	Asn	Asn	Val	Gln	Asp	Ile	Ile	Ala	Glu	Ile	Ile	Lys
		435					440					445		Lys
Glu	Ile	Asn	Glu	Lys	Ser	Asp	Gly	Phe	Thr	Ile	Thr	Asp	Ser	Glu
	450					455					460			Met
Lys	Arg	Ala	Phe	Glu	Ile	Tyr	Asn	Lys	Asp	Met	Leu	Ser	Asn	Asp
	465				470					475				Lys
Lys	Tyr	Thr	Leu	Asn	Asn	Ile	Pro	Ala	Ala	Tyr	Ala	Val	Met	Leu
			485					490						495
Asn	Met	Glu	Thr	Ile	Thr	Arg	Val	Tyr	Tyr	Gly	Asp	Leu	Tyr	Thr
		500						505					510	Asp
Asp	Gly	Asn	Tyr	Met	Glu	Ala	Lys	Ser	Pro	Tyr	Tyr	Asp	Thr	Ile
		515					520					525		Val
Asn	Leu	Met	Lys	Ser	Arg	Ile	Lys	Tyr	Val	Ser	Gly	Gly	Gln	Ala
		530				535					540			Gln
Arg	Ser	Tyr	Trp	Leu	Pro	Thr	Asp	Gly	Lys	Met	Asp	Lys	Ser	Asp
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Glu	Leu	Tyr	Arg	Thr	Asn	Glu	Val	Tyr	Thr	Ser	Val	Arg	Tyr	Gly
			565						570					575

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Asp	Ile	Met	Thr	Ala	Asp	Asp	Thr	Gln	Gly	Ser	Lys	Tyr	Ser	Arg	Thr	580	585	590
Ser	Gly	Gln	Val	Thr	Leu	Val	Val	Asn	Asn	Pro	Lys	Leu	Thr	Leu	Asp	595	600	605
Gln	Ser	Ala	Lys	Leu	Asn	Val	Val	Met	Gly	Lys	Ile	His	Ala	Asn	Gln	610	615	620
Lys	Tyr	Arg	Ala	Leu	Ile	Val	Gly	Thr	Pro	Asn	Gly	Ile	Lys	Asn	Phe	625	630	635
Thr	Ser	Asp	Ala	Glu	Ala	Ile	Ala	Ala	Gly	Tyr	Val	Lys	Glu	Thr	Asp	645	650	655
Gly	Asn	Gly	Val	Leu	Thr	Phe	Gly	Ala	Asn	Asp	Ile	Lys	Gly	Tyr	Glu	660	665	670
Thr	Phe	Asp	Met	Ser	Gly	Phe	Val	Ala	Val	Trp	Val	Pro	Val	Gly	Ala	675	680	685
Ser	Asp	Asp	Gln	Asp	Ile	Arg	Val	Ala	Ala	Ser	Thr	Ala	Ala	Lys	Lys	690	695	700
Glu	Gly	Glu	Leu	Thr	Leu	Lys	Ala	Thr	Glu	Ala	Tyr	Asp	Ser	Gln	Leu	705	710	715
Ile	Tyr	Glu	Gly	Phe	Ser	Asn	Phe	Gln	Thr	Ile	Pro	Asp	Gly	Ser	Asp	725	730	735
Pro	Ser	Val	Tyr	Thr	Asn	Arg	Lys	Ile	Ala	Glu	Asn	Val	Asp	Leu	Phe	740	745	750
Lys	Ser	Trp	Gly	Val	Thr	Ser	Phe	Glu	Met	Ala	Pro	Gln	Phe	Val	Ser	755	760	765
Ala	Asp	Asp	Gly	Thr	Phe	Leu	Asp	Ser	Val	Ile	Gln	Asn	Gly	Tyr	Ala	770	775	780
Phe	Ala	Asp	Arg	Tyr	Asp	Leu	Ala	Met	Ser	Lys	Asn	Asn	Lys	Tyr	Gly	785	790	795
Ser	Lys	Glu	Asp	Leu	Arg	Asn	Ala	Leu	Lys	Ala	Leu	His	Lys	Ala	Gly	805	810	815
Ile	Gln	Ala	Ile	Ala	Asp	Trp	Val	Pro	Asp	Gln	Ile	Tyr	Gln	Leu	Pro	820	825	830
Gly	Lys	Glu	Val	Val	Thr	Ala	Thr	Arg	Thr	Asp	Gly	Ala	Gly	Arg	Lys	835	840	845
Ile	Ser	Asp	Ala	Ile	Ile	Asp	His	Ser	Leu	Tyr	Val	Ala	Asn	Ser	Lys	850	855	860
Ser	Ser	Gly	Lys	Asp	Tyr	Gln	Ala	Lys	Tyr	Gly	Gly	Glu	Phe	Leu	Ala	865	870	875
Glu	Leu	Lys	Ala	Lys	Tyr	Pro	Glu	Met	Phe	Lys	Val	Asn	Met	Ile	Ser	885	890	895
Thr	Gly	Lys	Pro	Ile	Asp	Asp	Ser	Val	Lys	Leu	Lys	Gln	Trp	Lys	Ala	900	905	910
Glu	Tyr	Phe	Asn	Gly	Thr	Asn	Val	Leu	Asp	Arg	Gly	Val	Gly	Tyr	Val	915	920	925
Leu	Ser	Asp	Glu	Ala	Thr	Gly	Lys	Tyr	Phe	Thr	Val	Thr	Lys	Glu	Gly	930	935	940
Asn	Phe	Ile	Pro	Leu	Gln	Leu	Lys	Gly	Asn	Lys	Lys	Val	Ile	Thr	Gly	945	950	955
Phe	Ser	Ser	Asp	Gly	Lys	Gly	Ile	Thr	Tyr	Phe	Gly	Thr	Ser	Gly	Asn	965	970	975

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Gln	Ala	Lys	Ser	Ala	Phe	Val	Thr	Phe	Asn	Gly	Asn	Thr	Tyr	Tyr	Phe	980	985	990
Asp	Ala	Arg	Gly	His	Met	Val	Thr	Asn	Gly	Glu	Tyr	Ser	Pro	Asn	Gly	995	1000	1005
Lys	Asp	Val	Tyr	Arg	Phe	Leu	Pro	Asn	Gly	Ile	Met	Leu	Ser	Asn		1010	1015	1020
Ala	Phe	Tyr	Val	Asp	Gly	Asn	Gly	Asn	Thr	Tyr	Leu	Tyr	Asn	Ser		1025	1030	1035
Lys	Gly	Gln	Met	Tyr	Lys	Gly	Gly	Tyr	Ser	Lys	Phe	Asp	Val	Thr		1040	1045	1050
Glu	Thr	Lys	Asp	Gly	Lys	Glu	Ser	Lys	Val	Val	Lys	Phe	Arg	Tyr		1055	1060	1065
Phe	Thr	Asn	Glu	Gly	Val	Met	Ala	Lys	Gly	Val	Thr	Val	Val	Asp		1070	1075	1080
Gly	Phe	Thr	Gln	Tyr	Phe	Asn	Glu	Asp	Gly	Ile	Gln	Ser	Lys	Asp		1085	1090	1095
Glu	Leu	Val	Thr	Tyr	Asn	Gly	Lys	Thr	Tyr	Tyr	Phe	Glu	Ala	His		1100	1105	1110
Thr	Gly	Asn	Ala	Ile	Lys	Asn	Thr	Trp	Arg	Asn	Ile	Lys	Gly	Lys		1115	1120	1125
Trp	Tyr	His	Phe	Asp	Ala	Asn	Gly	Val	Ala	Ala	Thr	Gly	Ala	Gln		1130	1135	1140
Val	Ile	Asn	Gly	Gln	His	Leu	Tyr	Phe	Asn	Glu	Asp	Gly	Ser	Gln		1145	1150	1155
Val	Lys	Gly	Ser	Ile	Val	Lys	Asn	Ala	Asp	Gly	Thr	Phe	Ser	Lys		1160	1165	1170
Tyr	Lys	Asp	Ser	Ser	Gly	Asp	Leu	Val	Val	Asn	Glu	Phe	Phe	Thr		1175	1180	1185
Thr	Gly	Asp	Asn	Val	Trp	Tyr	Tyr	Ala	Gly	Ala	Asn	Gly	Lys	Thr		1190	1195	1200
Val	Thr	Gly	Ala	Gln	Val	Ile	Asn	Gly	Gln	His	Leu	Phe	Phe	Lys		1205	1210	1215
Glu	Asp	Gly	Ser	Gln	Val	Lys	Gly	Asp	Phe	Val	Lys	Asn	Ser	Asp		1220	1225	1230
Gly	Thr	Tyr	Ser	Lys	Tyr	Asp	Ala	Ala	Ser	Gly	Glu	Arg	Leu	Thr		1235	1240	1245
Asn	Glu	Phe	Phe	Thr	Thr	Gly	Asp	Asn	His	Trp	Tyr	Tyr	Ile	Gly		1250	1255	1260
Ala	Asn	Gly	Lys	Thr	Val	Thr	Gly	Glu	Val	Lys	Ile	Gly	Asp	Asp		1265	1270	1275
Thr	Tyr	Phe	Phe	Ala	Lys	Asp	Gly	Lys	Gln	Leu	Lys	Gly	Gln	Ile		1280	1285	1290
Val	Thr	Thr	Arg	Ser	Gly	Arg	Ile	Ser	Tyr	Tyr	Phe	Gly	Asp	Ser		1295	1300	1305
Gly	Lys	Lys	Ala	Ile	Ser	Thr	Trp	Val	Glu	Ile	Gln	Pro	Gly	Val		1310	1315	1320
Phe	Val	Phe	Phe	Asp	Lys	Asn	Gly	Leu	Ala	Tyr	Pro	Pro	Glu	Asn		1325	1330	1335
Met	Asn															1340		

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<210> SEQ ID NO 21

<400> SEQUENCE: 21

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<210> SEQ ID NO 22

<400> SEQUENCE: 22

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<210> SEQ ID NO 23

<400> SEQUENCE: 23

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<210> SEQ ID NO 24

<400> SEQUENCE: 24

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<210> SEQ ID NO 25

<211> LENGTH: 4308

<212> TYPE: DNA

<213> ORGANISM: Streptococcus sobrinus

<400> SEQUENCE: 25

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aaagtggacg cggacaagtc tagcagcgcc gttagccaaa atgcgacgat ctttgcggct	180
aacaatcgtg cgtatagcac ctctgctgag aactttgagg ccgttgataa ctatctgacg	240
gcagatagct ggtatcgtcc taaatctatt ctgaaagatg gcaagacgtg gaccgagtcg	300
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tctcaagcag atttgaccgc agcggcggag ctggtccagg cgcgtattga acagaaaatc	480
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cgcagtgga atggtgaaag cgagaagcgc tatgacgacc acctgcaaaa cgggtgctctg	600
aaattcgata atcagagcga cctgaccccg gacacccaga gcaactatcg cctgctgaat	660
cgcaccccgga ctaaccagac tggcagcctg gacagccgtt tcacctataa tgcgaacgat	720
ccgttggttg gctacgaatt tctgctggct aacgacgtgg ataatagcaa ccctgtggtg	780
caggcagaac aactgaactg gttgcattac ctggtgaatt ttggtagcat ttacgcgaaa	840
gatgcggatg caaacttcga ttccatccgt gtggacgcgc tggacaacgt cgatgcagat	900
ctgttgacga ttagcagcga ttacctgaag gcagcctatg gcattgacaa gaacaataag	960
aacgcgaaca accatgttag cattgttgag gcttgagcgc ataacgatac gccgtacctg	1020
cacgatgacg gtgataacct gatgaacatg gacaataagt tccgcttgag catgctgtgg	1080
agcctggcca agcgcgtgga caagcgcagc ggtctgaate ctctgattca taacagcctg	1140
gtggaccgtg aggttgatga ccgtgaagtg gaaacggttc cgagctactc ttttgcgcgt	1200
gcgcgatgatt ccgaggtcca agacattatc cgcgacatta tcaaggccga aatcaacccg	1260

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ttgctgctga cgaataaagg ttgatcccg cgtgtgtatt acggtgatat gttcaccgat	1440
gatggtcaat acatggcgaa caaaacgggt aactatgatg ccattgagtc gctgctgaaa	1500
gcgcgcatga agtacgttag cggcgggtcaa gcgatgcaaa actatcaaat cggcaatggt	1560
gagattctga ccagcgttcg ttatggtaag ggtgcattga agcaatccga caaggggtgac	1620
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gcaggtcttg tcaaacgcac cgatgaaaat gggtatttgt actttctgaa cgacgatctg	1860
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gctgacgac aggacattcg tgttgacgcg agcgacacgg ctacacgga cggttaagtc	1980
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aatggtcagc acctgtactt taaagaagat ggccaccaag ttaaagggtca gctggtcacc 3840
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aagaatggta aagtgttgac cggtttgcag accgtcgggtt cccagcgcgt gtactttgat 4140
gagaatggca ttcaagcaaa aggcгааagcg gttcgcacga gcgacggcaa aattcgtac 4200
ttcgacgaga acagcggtag catgatcacc aatcaatgga agtttgttta cggtaataac 4260
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<210> SEQ ID NO 26
<211> LENGTH: 1435
<212> TYPE: PRT
<213> ORGANISM: Streptococcus sobrinus

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<400> SEQUENCE: 26

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20     25     30
Thr Gly Ala Tyr Lys Asp Thr Ser Lys Val Asp Ala Asp Lys Ser Ser
35     40     45
Ser Ala Val Ser Gln Asn Ala Thr Ile Phe Ala Ala Asn Asn Arg Ala
50     55     60
Tyr Ser Thr Ser Ala Glu Asn Phe Glu Ala Val Asp Asn Tyr Leu Thr
65     70     75     80
Ala Asp Ser Trp Tyr Arg Pro Lys Ser Ile Leu Lys Asp Gly Lys Thr
85     90     95
Trp Thr Glu Ser Gly Lys Asp Asp Phe Arg Pro Leu Leu Met Ala Trp
100    105    110
Trp Pro Asp Thr Glu Thr Lys Arg Asn Tyr Val Asn Tyr Met Asn Leu
115    120    125
Val Val Gly Ile Asp Lys Thr Tyr Thr Ala Glu Thr Ser Gln Ala Asp
130    135    140
Leu Thr Ala Ala Ala Glu Leu Val Gln Ala Arg Ile Glu Gln Lys Ile
145    150    155    160
Thr Thr Glu Gln Asn Thr Lys Trp Leu Arg Glu Ala Ile Ser Ala Phe
165    170    175
Val Lys Thr Gln Pro Gln Trp Asn Gly Glu Ser Glu Lys Pro Tyr Asp
180    185    190
Asp His Leu Gln Asn Gly Ala Leu Lys Phe Asp Asn Gln Ser Asp Leu
195    200    205
Thr Pro Asp Thr Gln Ser Asn Tyr Arg Leu Leu Asn Arg Thr Pro Thr
210    215    220

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Asn	Gln	Thr	Gly	Ser	Leu	Asp	Ser	Arg	Phe	Thr	Tyr	Asn	Ala	Asn	Asp	
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Pro	Leu	Gly	Gly	Tyr	Glu	Phe	Leu	Leu	Ala	Asn	Asp	Val	Asp	Asn	Ser	
				245					250					255		
Asn	Pro	Val	Val	Gln	Ala	Glu	Gln	Leu	Asn	Trp	Leu	His	Tyr	Leu	Leu	
			260					265					270			
Asn	Phe	Gly	Ser	Ile	Tyr	Ala	Lys	Asp	Ala	Asp	Ala	Asn	Phe	Asp	Ser	
		275					280					285				
Ile	Arg	Val	Asp	Ala	Val	Asp	Asn	Val	Asp	Ala	Asp	Leu	Leu	Gln	Ile	
	290					295					300					
Ser	Ser	Asp	Tyr	Leu	Lys	Ala	Ala	Tyr	Gly	Ile	Asp	Lys	Asn	Asn	Lys	
305					310					315					320	
Asn	Ala	Asn	Asn	His	Val	Ser	Ile	Val	Glu	Ala	Trp	Ser	Asp	Asn	Asp	
				325					330					335		
Thr	Pro	Tyr	Leu	His	Asp	Asp	Gly	Asp	Asn	Leu	Met	Asn	Met	Asp	Asn	
			340					345						350		
Lys	Phe	Arg	Leu	Ser	Met	Leu	Trp	Ser	Leu	Ala	Lys	Pro	Leu	Asp	Lys	
		355					360					365				
Arg	Ser	Gly	Leu	Asn	Pro	Leu	Ile	His	Asn	Ser	Leu	Val	Asp	Arg	Glu	
	370					375						380				
Val	Asp	Asp	Arg	Glu	Val	Glu	Thr	Val	Pro	Ser	Tyr	Ser	Phe	Ala	Arg	
385					390					395					400	
Ala	His	Asp	Ser	Glu	Val	Gln	Asp	Ile	Ile	Arg	Asp	Ile	Ile	Lys	Ala	
				405				410						415		
Glu	Ile	Asn	Pro	Asn	Ser	Phe	Gly	Tyr	Ser	Phe	Thr	Gln	Glu	Glu	Ile	
			420					425					430			
Asp	Gln	Ala	Phe	Lys	Ile	Tyr	Asn	Glu	Asp	Leu	Lys	Lys	Thr	Asp	Lys	
		435					440					445				
Lys	Tyr	Thr	His	Tyr	Asn	Val	Pro	Leu	Ser	Tyr	Thr	Leu	Leu	Leu	Thr	
	450					455					460					
Asn	Lys	Gly	Ser	Ile	Pro	Arg	Val	Tyr	Tyr	Gly	Asp	Met	Phe	Thr	Asp	
465					470					475					480	
Asp	Gly	Gln	Tyr	Met	Ala	Asn	Lys	Thr	Val	Asn	Tyr	Asp	Ala	Ile	Glu	
				485				490						495		
Ser	Leu	Leu	Lys	Ala	Arg	Met	Lys	Tyr	Val	Ser	Gly	Gly	Gln	Ala	Met	
		500						505					510			
Gln	Asn	Tyr	Gln	Ile	Gly	Asn	Gly	Glu	Ile	Leu	Thr	Ser	Val	Arg	Tyr	
		515					520					525				
Gly	Lys	Gly	Ala	Leu	Lys	Gln	Ser	Asp	Lys	Gly	Asp	Ala	Thr	Thr	Arg	
	530					535					540					
Thr	Ser	Gly	Val	Gly	Val	Val	Met	Gly	Asn	Gln	Pro	Asn	Phe	Ser	Leu	
545					550					555					560	
Asp	Gly	Lys	Val	Val	Ala	Leu	Asn	Met	Gly	Ala	Ala	His	Ala	Asn	Gln	
				565					570					575		
Glu	Tyr	Arg	Ala	Leu	Met	Val	Ser	Thr	Lys	Asp	Gly	Val	Ala	Thr	Tyr	
		580						585					590			
Ala	Thr	Asp	Ala	Asp	Ala	Ser	Lys	Ala	Gly	Leu	Val	Lys	Arg	Thr	Asp	
		595					600					605				
Glu	Asn	Gly	Tyr	Leu	Tyr	Phe	Leu	Asn	Asp	Asp	Leu	Lys	Gly	Val	Ala	
	610					615					620					

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Asn	Pro	Gln	Val	Ser	Gly	Phe	Leu	Gln	Val	Trp	Val	Pro	Val	Gly	Ala
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			645						650					655	
Asp	Gly	Lys	Ser	Leu	His	Gln	Asp	Ala	Ala	Met	Asp	Ser	Arg	Val	Met
		660						665					670		
Phe	Glu	Gly	Phe	Ser	Asn	Phe	Gln	Ser	Phe	Ala	Thr	Lys	Glu	Glu	Glu
	675						680					685			
Tyr	Thr	Asn	Val	Val	Ile	Ala	Asn	Asn	Val	Asp	Lys	Phe	Val	Ser	Trp
690					695						700				
Gly	Ile	Thr	Asp	Phe	Glu	Met	Ala	Pro	Gln	Tyr	Val	Ser	Ser	Thr	Asp
705					710					715					720
Gly	Gln	Phe	Leu	Asp	Ser	Val	Ile	Gln	Asn	Gly	Tyr	Ala	Phe	Thr	Asp
			725						730					735	
Arg	Tyr	Asp	Leu	Gly	Met	Ser	Lys	Ala	Asn	Lys	Tyr	Gly	Thr	Ala	Asp
		740						745					750		
Gln	Leu	Val	Lys	Ala	Ile	Lys	Ala	Leu	His	Ala	Lys	Gly	Leu	Lys	Val
	755						760					765			
Met	Ala	Asp	Trp	Val	Pro	Asp	Gln	Met	Tyr	Thr	Phe	Pro	Lys	Gln	Glu
770						775					780				
Val	Val	Thr	Val	Thr	Arg	Thr	Asp	Lys	Phe	Gly	Lys	Pro	Ile	Ala	Gly
785					790					795					800
Ser	Gln	Ile	Asn	His	Ser	Leu	Tyr	Val	Thr	Asp	Thr	Lys	Ser	Ser	Gly
			805						810					815	
Asp	Asp	Tyr	Gln	Ala	Lys	Tyr	Gly	Gly	Ala	Phe	Leu	Asp	Glu	Leu	Lys
			820					825					830		
Glu	Lys	Tyr	Pro	Glu	Leu	Phe	Thr	Lys	Lys	Gln	Ile	Ser	Thr	Gly	Gln
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850						855					860				
Asn	Gly	Ser	Asn	Ile	Leu	Gly	Arg	Gly	Ala	Asp	Tyr	Val	Leu	Ser	Asp
865				870						875					880
Gln	Val	Ser	Asn	Lys	Tyr	Phe	Asn	Val	Ala	Ser	Asp	Thr	Leu	Phe	Leu
			885						890					895	
Pro	Ser	Ser	Leu	Leu	Gly	Lys	Val	Val	Glu	Ser	Gly	Ile	Arg	Tyr	Asp
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Gly	Lys	Gly	Tyr	Ile	Tyr	Asn	Ser	Ser	Ala	Thr	Gly	Asp	Gln	Val	Lys
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930						935					940				
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Phe	Leu	Glu	Asn	Gly	Thr	Ala	Leu	Arg	Asn	Thr	Ile	Tyr	Thr	Asp	Ala
			965						970					975	
Gln	Gly	Asn	Ser	His	Tyr	Tyr	Ala	Asn	Asp	Gly	Lys	Arg	Tyr	Glu	Asn
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		995					1000					1005			
Met	Ala	Val	Gly	Leu	Thr	Thr	Val	Asp	Gly	Asn	Val	Gln	Tyr	Phe	
1010						1015						1020			
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1025	1030	1035
Asp Gly Lys Val Arg Tyr Phe 1040	Asp Gln His Asn Gly Asn Ala Val 1045	1050
Thr Asn Thr Phe Ile Ala Asp 1055	Lys Thr Gly His Trp Tyr Tyr Leu 1060	1065
Gly Lys Asp Gly Val Ala Val 1070	Thr Gly Ala Gln Thr Val Gly Lys 1075	1080
Gln Lys Leu Tyr Phe Glu Ala 1085	Asn Gly Glu Gln Val Lys Gly Asp 1090	1095
Phe Val Thr Ser His Glu Gly 1100	Lys Leu Tyr Phe Tyr Asp Val Asp 1105	1110
Ser Gly Asp Met Trp Thr Asp 1115	Thr Phe Ile Glu Asp Lys Ala Gly 1120	1125
Asn Trp Phe Tyr Leu Gly Lys 1130	Asp Gly Ala Ala Val Ser Gly Ala 1135	1140
Gln Thr Ile Arg Gly Gln Lys 1145	Leu Tyr Phe Lys Ala Tyr Gly Gln 1150	1155
Gln Val Lys Gly Asp Ile Val 1160	Lys Gly Thr Asp Gly Lys Ile Arg 1165	1170
Tyr Tyr Asp Ala Lys Ser Gly 1175	Glu Gln Val Phe Asn Lys Thr Val 1180	1185
Lys Ala Ala Asp Gly Lys Thr 1190	Tyr Val Ile Gly Asn Asn Gly Val 1195	1200
Ala Val Asp Pro Ser Val Val 1205	Lys Gly Gln Thr Phe Lys Asp Ala 1210	1215
Ser Gly Ala Leu Arg Phe Tyr 1220	Asn Leu Lys Gly Gln Leu Val Thr 1225	1230
Gly Ser Gly Trp Tyr Glu Thr 1235	Ala Asn His Asp Trp Val Tyr Ile 1240	1245
Gln Ser Gly Lys Ala Leu Thr 1250	Gly Glu Gln Thr Ile Asn Gly Gln 1255	1260
His Leu Tyr Phe Lys Glu Asp 1265	Gly His Gln Val Lys Gly Gln Leu 1270	1275
Val Thr Arg Thr Asp Gly Lys 1280	Val Arg Tyr Tyr Asp Ala Asn Ser 1285	1290
Gly Asp Gln Ala Phe Asn Lys 1295	Ser Val Thr Val Asn Gly Lys Thr 1300	1305
Tyr Tyr Phe Gly Asn Asp Gly 1310	Thr Ala Gln Thr Ala Gly Asn Pro 1315	1320
Lys Gly Gln Ile Phe Lys Asp 1325	Gly Ser Val Leu Arg Phe Tyr Ser 1330	1335
Met Glu Gly Gln Leu Val Ile 1340	Gly Ser Gly Trp Tyr Ser Asn Ala 1345	1350
Gln Gly Gln Trp Leu Tyr Val 1355	Lys Asn Gly Lys Val Leu Thr Gly 1360	1365
Leu Gln Thr Val Gly Ser Gln 1370	Arg Val Tyr Phe Asp Glu Asn Gly 1375	1380
Ile Gln Ala Lys Gly Lys Ala 1385	Val Arg Thr Ser Asp Gly Lys Ile 1390	1395
Arg Tyr Phe Asp Glu Asn Ser 1400	Gly Ser Met Ile Thr Asn Gln Trp 1405	1410

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Lys Phe Val Tyr Gly Gln Tyr Tyr Tyr Phe Gly Asn Asp Gly Ala
 1415 1420 1425

Ala Ile Tyr Arg Gly Trp Asn
 1430 1435

<210> SEQ ID NO 27

<211> LENGTH: 4023

<212> TYPE: DNA

<213> ORGANISM: Streptococcus salivarius PS4

<400> SEQUENCE: 27

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atgattgacg gcaaatacta ctacgtaaac aaagatggct cgcacaaaga gaatttcgca    60
attaccgtga atggtcaggt gttgtatttc ggtaaggacg gtgcattgac gtctagcagc    120
acctacagct ttacgcaggg caccaccaac atcgttgatg gcttttagcaa aaacaaccgt    180
gcgtacgatt ccagcgaggg gagctttgaa ctgatecgac gttatctgac cgcggactcc    240
tggtatcgtc cggtgagcat tatcaaggac ggcgttacgt ggcaagccag caccaagag    300
gactttcgcc cgctgctgat ggcttgggtg ccgaatgttg acaccaggt caactacctg    360
aattacatgt cgaaggtggt taacctggac gcgaagtata cgagaccga caaacagggt    420
gacctgaatc gcgcagccaa ggacattcag gttaagattg agcaaaagat tcaggccgag    480
aagagcactc aatggctgcg tgaagcgatt tcggccttcg tcaaaaccca gccgcagtgg    540
aataaagaaa cggagaactt ctccaagggt ggtggtgagg atcatctgca aggtggtgca    600
ctgctgtacg ttaacgaccc gcgtaccccg tgggctaact ccaactaccg cctgctgaat    660
cgtaactgca ccaaccagac cggcacgacg gacaagagcg ttctggacga acagagcgat    720
cctaaccaca tgggcgggctt cgattttctg ctggcgaatg acgtcgatac cagcaatccg    780
gtggtgacag cggaacaact gaatcagatc cactacctga tgaattgggg ttccattggt    840
atgggcgaca aagatgcaaa ctctgatggt atccgcgtgg acgcggtcga taacgttgac    900
gcagatatgc tgcaactgta caccaactac ttctgtgagt attatggcgt gaacaaaagc    960
gaggcaaacg ctttggcgca catctcgggt ctggaagcgt ggagcttgaa tgataatcac   1020
tataatgaca agactgacgg tgccggccctg gcgatggaga acaaacagcg tttggccctg   1080
ctgtttagct tggcgaaacc gatcaaagaa cgtacccctg cggtgagccc gctgtacaac   1140
aacactttca acacgacgca gcgtgacgaa aagaccgatt ggattaacaa agacggtagc   1200
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tacggcgacg cgtccggcaa ttatgtgttc attcgcgccc acgataacaa cgtccaagac   1320
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gacgccgaaa tgaaaaaggc attcgaaatc tacaacaaag atatgctgtc ctctgataag   1440
aaatacaccc tgaacaacat ccagcgggcc tacgcgggtg tgctgcaaaa catggaaacc   1500
attactcgtg tgtattacgg cgatctgtat accgacgatg gccattacat ggaaaccaag   1560
agcccgtact acgacaccat tgtgaacctg atgaagaacc gtatcaaata cgtgtccggt   1620
ggtcaagcgc aacgttccta ttggctgccc accgacggta agatggataa aagcgatgtc   1680
gaactgtatc gcaccaacga ggtgtacacc agcgtccgtt acgtaagga catcatgact   1740
gccgatgaca cccaaggtag caagtacagc cgtaccagcg gtcagggtgac cctggtggtg   1800
aacaaccgga agctgtcttt ggataagagc gcgaagctgg acgtcgaaat gggcaagatc   1860

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catgcaaaacc	agaaataaccg	tgctctgac	gtgggtacgc	cgaacggcat	caaaaacttc	1920
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ctgaccttcg	gtgcaaatga	catcaaaggt	tacgaaacgt	ttgacatgag	cggtttcgtt	2040
gcagtttggg	ttccggtagg	tgcaagcgat	gatcaagaca	tccgtgtcgc	cgcaagcacc	2100
gcggcaaaga	aagaaggtga	gctgactttg	aaggcaactg	aggcgtatga	ctctcagctg	2160
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caaatgtaca	aaggtgggtta	tagcaaatc	gacgttacgg	aaaccaaaga	tggtaaagag	3180
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ttcttcgcaa	aagatggcaa	gcagctgaag	ggccagatcg	tgacgacccg	cagcggctcg	3900
atcagctact	acttcggcga	ctctggttaag	aaggcgatta	gcacctgggt	ggagattcag	3960
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taa						4023

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<210> SEQ ID NO 28
<211> LENGTH: 1340
<212> TYPE: PRT
<213> ORGANISM: *Streptococcus salivarius* PS4

<400> SEQUENCE: 28

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Glu Asn Phe Ala Ile Thr Val Asn Gly Gln Leu Leu Tyr Phe Gly Lys
20 25 30

Asp Gly Ala Leu Thr Ser Ser Ser Thr Tyr Ser Phe Thr Gln Gly Thr
35 40 45

Thr Asn Ile Val Asp Gly Phe Ser Lys Asn Asn Arg Ala Tyr Asp Ser
50 55 60

Ser Glu Ala Ser Phe Glu Leu Ile Asp Gly Tyr Leu Thr Ala Asp Ser
65 70 75 80

Trp Tyr Arg Pro Val Ser Ile Ile Lys Asp Gly Val Thr Trp Gln Ala
85 90 95

Ser Thr Lys Glu Asp Phe Arg Pro Leu Leu Met Ala Trp Trp Pro Asn
100 105 110

Val Asp Thr Gln Val Asn Tyr Leu Asn Tyr Met Ser Lys Val Phe Asn
115 120 125

Leu Asp Ala Lys Tyr Thr Ser Thr Asp Lys Gln Val Asp Leu Asn Arg
130 135 140

Ala Ala Lys Asp Ile Gln Val Lys Ile Glu Gln Lys Ile Gln Ala Glu
145 150 155 160

Lys Ser Thr Gln Trp Leu Arg Glu Ala Ile Ser Ala Phe Val Lys Thr
165 170 175

Gln Pro Gln Trp Asn Lys Glu Thr Glu Asn Phe Ser Lys Gly Gly Gly
180 185 190

Glu Asp His Leu Gln Gly Gly Ala Leu Leu Tyr Val Asn Asp Pro Arg
195 200 205

Thr Pro Trp Ala Asn Ser Asn Tyr Arg Leu Leu Asn Arg Thr Ala Thr
210 215 220

Asn Gln Thr Gly Thr Ile Asp Lys Ser Val Leu Asp Glu Gln Ser Asp
225 230 235 240

Pro Asn His Met Gly Gly Phe Asp Phe Leu Leu Ala Asn Asp Val Asp
245 250 255

Thr Ser Asn Pro Val Val Gln Ala Glu Gln Leu Asn Gln Ile His Tyr
260 265 270

Leu Met Asn Trp Gly Ser Ile Val Met Gly Asp Lys Asp Ala Asn Phe
275 280 285

Asp Gly Ile Arg Val Asp Ala Val Asp Asn Val Asp Ala Asp Met Leu
290 295 300

Gln Leu Tyr Thr Asn Tyr Phe Arg Glu Tyr Tyr Gly Val Asn Lys Ser
305 310 315 320

Glu Ala Asn Ala Leu Ala His Ile Ser Val Leu Glu Ala Trp Ser Leu
325 330 335

Asn Asp Asn His Tyr Asn Asp Lys Thr Asp Gly Ala Ala Leu Ala Met
340 345 350

Glu Asn Lys Gln Arg Leu Ala Leu Leu Phe Ser Leu Ala Lys Pro Ile
355 360 365

Lys 370	Arg	Thr	Pro	Ala	Val 375	Ser	Pro	Leu	Tyr	Asn 380	Asn	Thr	Phe	Asn	
Thr 385	Thr	Gln	Arg	Asp	Glu 390	Lys	Thr	Asp	Trp	Ile 395	Asn	Lys	Asp	Gly	Ser 400
Lys	Ala	Tyr	Asn	Glu 405	Asp	Gly	Thr	Val	Lys 410	Gln	Ser	Thr	Ile	Gly 415	Lys
Tyr	Asn	Glu	Lys 420	Tyr	Gly	Asp	Ala	Ser 425	Gly	Asn	Tyr	Val	Phe 430	Ile	Arg
Ala	His 435	Asp	Asn	Asn	Val	Gln	Asp 440	Ile	Ile	Ala	Glu	Ile 445	Ile	Lys	Lys
Glu 450	Ile	Asn	Pro	Lys	Ser	Asp 455	Gly	Phe	Thr	Ile	Thr 460	Asp	Ala	Glu	Met
Lys 465	Lys	Ala	Phe	Glu	Ile 470	Tyr	Asn	Lys	Asp	Met 475	Leu	Ser	Ser	Asp	Lys 480
Lys	Tyr	Thr	Leu 485	Asn	Asn	Ile	Pro	Ala	Ala 490	Tyr	Ala	Val	Met	Leu 495	Gln
Asn	Met	Glu	Thr 500	Ile	Thr	Arg	Val	Tyr 505	Tyr	Gly	Asp	Leu 510	Tyr	Thr	Asp
Asp	Gly	His 515	Tyr	Met	Glu	Thr	Lys 520	Ser	Pro	Tyr	Tyr	Asp 525	Thr	Ile	Val
Asn 530	Leu	Met	Lys	Asn	Arg	Ile 535	Lys	Tyr	Val	Ser	Gly 540	Gly	Gln	Ala	Gln
Arg 545	Ser	Tyr	Trp	Leu	Pro 550	Thr	Asp	Gly	Lys	Met 555	Asp	Lys	Ser	Asp	Val 560
Glu	Leu	Tyr	Arg	Thr 565	Asn	Glu	Val	Tyr	Thr 570	Ser	Val	Arg	Tyr	Gly 575	Lys
Asp	Ile	Met	Thr 580	Ala	Asp	Asp	Thr	Gln 585	Gly	Ser	Lys	Tyr	Ser 590	Arg	Thr
Ser	Gly	Gln 595	Val	Thr	Leu	Val	Val 600	Asn	Asn	Pro	Lys	Leu 605	Ser	Leu	Asp
Lys 610	Ser	Ala	Lys	Leu	Asp	Val 615	Glu	Met	Gly	Lys	Ile 620	His	Ala	Asn	Gln
Lys 625	Tyr	Arg	Ala	Leu	Ile 630	Val	Gly	Thr	Pro	Asn 635	Gly	Ile	Lys	Asn	Phe 640
Thr	Ser	Asp	Ala 645	Glu	Ala	Ile	Ala	Ala	Gly 650	Tyr	Val	Lys	Glu	Thr 655	Asp
Gly	Asn	Gly	Val 660	Leu	Thr	Phe	Gly	Ala 665	Asn	Asp	Ile	Lys	Gly 670	Tyr	Glu
Thr	Phe 675	Asp	Met	Ser	Gly	Phe	Val 680	Ala	Val	Trp	Val	Pro 685	Val	Gly	Ala
Ser 690	Asp	Asp	Gln	Asp	Ile	Arg 695	Val	Ala	Ala	Ser	Thr 700	Ala	Ala	Lys	Lys
Glu 705	Gly	Glu	Leu	Thr	Leu 710	Lys	Ala	Thr	Glu	Ala 715	Tyr	Asp	Ser	Gln	Leu 720
Ile	Tyr	Glu	Gly 725	Phe	Ser	Asn	Phe	Gln	Thr 730	Ile	Pro	Asp	Gly	Ser 735	Asp
Pro	Ser	Val	Tyr 740	Thr	Asn	Arg	Lys	Ile 745	Ala	Glu	Asn	Val 750	Asp	Leu	Phe
Lys	Ser	Trp 755	Gly	Val	Thr	Ser	Phe 760	Glu	Met	Ala	Pro	Gln 765	Phe	Val	Ser
Ala	Asp	Asp	Gly	Thr	Phe	Leu	Asp	Ser	Val	Ile	Gln	Asn	Gly	Tyr	Ala

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770	775	780
Phe Ala Asp Arg Tyr Asp	Leu Ala Met Ser Lys	Asn Asn Lys Tyr Gly
785	790	795 800
Ser Lys Glu Asp Leu Arg	Asn Ala Leu Lys Ala	Leu His Lys Ala Gly
	805	810 815
Ile Gln Ala Ile Ala Asp	Trp Val Pro Asp Gln	Ile Tyr Gln Leu Pro
	820	825 830
Gly Lys Glu Val Val Thr	Ala Thr Arg Thr Asp	Gly Ala Gly Arg Lys
	835	840 845
Ile Ser Asp Ala Ile Ile	Asp His Ser Leu Tyr	Val Ala Asn Ser Lys
	850	855 860
Ser Ser Gly Lys Asp Tyr	Gln Ala Lys Tyr Gly	Gly Glu Phe Leu Ala
865	870	875 880
Glu Leu Lys Ala Lys Tyr	Pro Glu Met Phe Lys	Val Asn Met Ile Ser
	885	890 895
Thr Gly Lys Pro Ile Asp	Asp Ser Val Lys Leu	Lys Gln Trp Lys Ala
	900	905 910
Glu Tyr Phe Asn Gly Thr	Asn Val Leu Asp Arg	Gly Val Gly Tyr Val
	915	920 925
Leu Ser Asp Glu Ala Thr	Gly Lys Tyr Phe Thr	Val Thr Lys Glu Gly
	930	935 940
Asn Phe Ile Pro Leu Gln	Leu Lys Gly Asn Glu	Lys Val Ile Thr Gly
945	950	955 960
Phe Ser Ser Asp Gly Lys	Gly Ile Thr Tyr Phe	Gly Thr Ser Gly Asn
	965	970 975
Gln Ala Lys Ser Ala Phe	Val Thr Phe Asn Gly	Asn Thr Tyr Tyr Phe
	980	985 990
Asp Ala Arg Gly His Met	Val Thr Asn Gly Glu	Tyr Ser Pro Asn Gly
	995	1000 1005
Lys Asp Val Tyr Arg Phe	Leu Pro Asn Gly Ile	Met Leu Ser Asn
	1010	1015 1020
Ala Phe Tyr Val Asp Gly	Asn Gly Asn Thr Tyr	Leu Tyr Asn Ser
	1025	1030 1035
Lys Gly Gln Met Tyr Lys	Gly Gly Tyr Ser Lys	Phe Asp Val Thr
	1040	1045 1050
Glu Thr Lys Asp Gly Lys	Glu Ser Lys Val Val	Lys Phe Arg Tyr
	1055	1060 1065
Phe Thr Asn Glu Gly Val	Met Ala Lys Gly Val	Thr Val Val Asp
	1070	1075 1080
Gly Phe Thr Gln Tyr Phe	Asn Glu Asp Gly Ile	Gln Ser Lys Asp
	1085	1090 1095
Glu Leu Val Thr Tyr Asn	Gly Lys Thr Tyr Tyr	Phe Glu Ala His
	1100	1105 1110
Thr Gly Asn Ala Ile Lys	Asn Thr Trp Arg Asn	Ile Lys Gly Lys
	1115	1120 1125
Trp Tyr His Phe Asp Ala	Asn Gly Val Ala Ala	Thr Gly Ala Gln
	1130	1135 1140
Val Ile Asn Gly Gln His	Leu Tyr Phe Asn Glu	Asp Gly Ser Gln
	1145	1150 1155
Val Lys Gly Gly Val Val	Lys Asn Ala Asp Gly	Thr Phe Ser Lys
	1160	1165 1170

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Tyr	Lys	Asp	Gly	Ser	Gly	Asp	Leu	Val	Val	Asn	Glu	Phe	Phe	Thr
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Thr	Gly	Asp	Asn	Val	Trp	Tyr	Tyr	Ala	Gly	Ala	Asn	Gly	Lys	Thr
1190						1195					1200			
Val	Thr	Gly	Ala	Gln	Val	Ile	Asn	Gly	Gln	His	Leu	Phe	Phe	Lys
1205						1210					1215			
Glu	Asp	Gly	Ser	Gln	Val	Lys	Gly	Asp	Phe	Val	Lys	Asn	Ser	Asp
1220						1225					1230			
Gly	Thr	Tyr	Ser	Lys	Tyr	Asp	Ala	Ala	Ser	Gly	Glu	Arg	Leu	Thr
1235						1240					1245			
Asn	Glu	Phe	Phe	Thr	Thr	Gly	Asp	Asn	His	Trp	Tyr	Tyr	Ile	Gly
1250						1255					1260			
Ala	Asn	Gly	Lys	Thr	Val	Thr	Gly	Glu	Val	Lys	Ile	Gly	Asp	Asp
1265						1270					1275			
Thr	Tyr	Phe	Phe	Ala	Lys	Asp	Gly	Lys	Gln	Leu	Lys	Gly	Gln	Ile
1280						1285					1290			
Val	Thr	Thr	Arg	Ser	Gly	Arg	Ile	Ser	Tyr	Tyr	Phe	Gly	Asp	Ser
1295						1300					1305			
Gly	Lys	Lys	Ala	Ile	Ser	Thr	Trp	Val	Glu	Ile	Gln	Pro	Gly	Val
1310						1315					1320			
Phe	Val	Phe	Phe	Asp	Lys	Asn	Gly	Leu	Ala	Tyr	Pro	Pro	Glu	Asn
1325						1330					1335			
Met	Asn													
1340														

<210> SEQ ID NO 29

<211> LENGTH: 4026

<212> TYPE: DNA

<213> ORGANISM: Streptococcus salivarius K12

<400> SEQUENCE: 29

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acgcacagct tcacgcggg tactacgaat attgtggacg gtttctcgat caacaaccgt	180
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gattttcgtc cgctgttgat ggctgtgtgg ccgaacgttg ataccaggt gaactatctg	360
aactatatgt ccaaggtctt taacctggaa gccaaagtaca ccagcaccga taaacaggct	420
gatctgaacc gtgctgcaaa ggatatccag gtcaagatcg aacagaagat ccaggcgga	480
aagagcacgc agtggctgcg tgagactatc tccgcgtttg ttaaaaccca gccgcaatgg	540
aacaaagaga ctgagaatta ctccaagggt ggtggcgaag atcatctgca aggcggtg	600
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ccaaatcaca tgggtggctt cgacttctct ctggcaaacg atgtggatct gagcaatcct	780
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ctgttctctc	tggccaagcc	gatcaaagat	cgtactccgg	cagtgcagcc	actgtataac	1140
aatactttca	ataccaccca	acgtgacttc	aagacggatt	ggattaacaa	ggacggtagc	1200
accgcctaca	atgaggatgg	caccgcgaaa	caatctacca	tcgtaagta	caatgagaaa	1260
tatggtgatg	caagcggtaa	ctatgtgttt	attcgtgccc	atgacaataa	cgtccaagac	1320
attattgcgg	agatcattaa	gaaagaaatc	aataagaaga	gcgatggttt	taccatcagc	1380
gatagcgaaa	tgaaacaggc	gttcgaaatc	tacaacaaag	atatgctgag	cagcaataag	1440
aaatacactc	tgaataacat	tccggcagcg	tacgcctga	tgctgcaaaa	catggagact	1500
atcacccgtg	tgtattatgg	tgacctgtac	accgacgacg	gtcactatat	ggaaaccaag	1560
agcccgatc	atgacaccat	tgtgaacctg	atgaaaaacc	gtatcaagta	cgtttctggt	1620
ggccaggccc	aacgctccta	ttggctgccc	accgacggta	aaatggacaa	tagcgatgtc	1680
gaactgtacc	gtactagcga	ggctctatac	agcgttcgct	acggtaagga	cattatgacg	1740
gcggatgaca	ccgagggtag	caagtactcc	cgcacgagcg	gtcagggttac	cctgggtgtt	1800
aacaacccga	agctgactct	gcataaaagc	gccaaactga	acgtcgagat	gggtaagatc	1860
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<210> SEQ ID NO 30

<211> LENGTH: 1341

<212> TYPE: PRT

<213> ORGANISM: Streptococcus salivarius K12

<400> SEQUENCE: 30

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Glu Asn Phe Ala Ile Thr Val Asn Gly Gln Leu Leu Tyr Phe Gly Lys
20          25          30

Asp Gly Ala Leu Thr Ser Ser Ser Thr His Ser Phe Thr Pro Gly Thr
35          40          45

Thr Asn Ile Val Asp Gly Phe Ser Ile Asn Asn Arg Ala Tyr Asp Ser
50          55          60

Ser Glu Ala Ser Phe Glu Leu Ile Asn Gly Tyr Leu Thr Ala Asp Ser
65          70          75          80

Trp Tyr Arg Pro Val Ser Ile Ile Lys Asp Gly Val Thr Trp Gln Ala
85          90          95

Ser Thr Ala Glu Asp Phe Arg Pro Leu Leu Met Ala Trp Trp Pro Asn
100         105         110

Val Asp Thr Gln Val Asn Tyr Leu Asn Tyr Met Ser Lys Val Phe Asn
115         120         125

Leu Glu Ala Lys Tyr Thr Ser Thr Asp Lys Gln Ala Asp Leu Asn Arg
130         135         140

Ala Ala Lys Asp Ile Gln Val Lys Ile Glu Gln Lys Ile Gln Ala Glu
145         150         155         160

Lys Ser Thr Gln Trp Leu Arg Glu Thr Ile Ser Ala Phe Val Lys Thr
165         170         175

Gln Pro Gln Trp Asn Lys Glu Thr Glu Asn Tyr Ser Lys Gly Gly Gly
180         185         190

Glu Asp His Leu Gln Gly Gly Ala Leu Leu Tyr Val Asn Asp Ser Arg
195         200         205

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Thr	Pro	Trp	Ala	Asn	Ser	Asn	Tyr	Arg	Leu	Leu	Asn	Arg	Thr	Ala	Thr
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Asn	Gln	Thr	Gly	Thr	Ile	Asn	Lys	Ser	Val	Leu	Asp	Glu	Gln	Ser	Asp
225					230					235					240
Pro	Asn	His	Met	Gly	Gly	Phe	Asp	Phe	Leu	Leu	Ala	Asn	Asp	Val	Asp
			245						250					255	
Leu	Ser	Asn	Pro	Val	Val	Gln	Ala	Glu	Gln	Leu	Asn	Gln	Ile	His	Tyr
			260					265					270		
Leu	Met	Asn	Trp	Gly	Ser	Ile	Val	Met	Gly	Asp	Lys	Asp	Ala	Asn	Phe
		275					280					285			
Asp	Gly	Ile	Arg	Val	Asp	Ala	Val	Asp	Asn	Val	Asn	Ala	Asp	Met	Leu
290						295					300				
Gln	Leu	Tyr	Thr	Asn	Tyr	Phe	Arg	Glu	Tyr	Tyr	Gly	Val	Asn	Lys	Ser
305					310					315					320
Glu	Ala	Gln	Ala	Leu	Ala	His	Ile	Ser	Val	Leu	Glu	Ala	Trp	Ser	Leu
				325					330					335	
Asn	Asp	Asn	His	Tyr	Asn	Asp	Lys	Thr	Asp	Gly	Ala	Ala	Leu	Ala	Met
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Glu	Asn	Lys	Gln	Arg	Leu	Ala	Leu	Leu	Phe	Ser	Leu	Ala	Lys	Pro	Ile
		355					360					365			
Lys	Asp	Arg	Thr	Pro	Ala	Val	Ser	Pro	Leu	Tyr	Asn	Asn	Thr	Phe	Asn
370						375					380				
Thr	Thr	Gln	Arg	Asp	Phe	Lys	Thr	Asp	Trp	Ile	Asn	Lys	Asp	Gly	Ser
385					390					395					400
Thr	Ala	Tyr	Asn	Glu	Asp	Gly	Thr	Ala	Lys	Gln	Ser	Thr	Ile	Gly	Lys
				405					410					415	
Tyr	Asn	Glu	Lys	Tyr	Gly	Asp	Ala	Ser	Gly	Asn	Tyr	Val	Phe	Ile	Arg
			420					425					430		
Ala	His	Asp	Asn	Asn	Val	Gln	Asp	Ile	Ile	Ala	Glu	Ile	Ile	Lys	Lys
		435					440					445			
Glu	Ile	Asn	Lys	Lys	Ser	Asp	Gly	Phe	Thr	Ile	Ser	Asp	Ser	Glu	Met
450						455					460				
Lys	Gln	Ala	Phe	Glu	Ile	Tyr	Asn	Lys	Asp	Met	Leu	Ser	Ser	Asn	Lys
465					470					475					480
Lys	Tyr	Thr	Leu	Asn	Asn	Ile	Pro	Ala	Ala	Tyr	Ala	Val	Met	Leu	Gln
				485					490					495	
Asn	Met	Glu	Thr	Ile	Thr	Arg	Val	Tyr	Tyr	Gly	Asp	Leu	Tyr	Thr	Asp
			500					505					510		
Asp	Gly	His	Tyr	Met	Glu	Thr	Lys	Ser	Pro	Tyr	His	Asp	Thr	Ile	Val
		515						520				525			
Asn	Leu	Met	Lys	Asn	Arg	Ile	Lys	Tyr	Val	Ser	Gly	Gly	Gln	Ala	Gln
530						535					540				
Arg	Ser	Tyr	Trp	Leu	Pro	Thr	Asp	Gly	Lys	Met	Asp	Asn	Ser	Asp	Val
545					550					555					560
Glu	Leu	Tyr	Arg	Thr	Ser	Glu	Val	Tyr	Thr	Ser	Val	Arg	Tyr	Gly	Lys
				565					570					575	
Asp	Ile	Met	Thr	Ala	Asp	Asp	Thr	Glu	Gly	Ser	Lys	Tyr	Ser	Arg	Thr
			580					585					590		
Ser	Gly	Gln	Val	Thr	Leu	Val	Val	Asn	Asn	Pro	Lys	Leu	Thr	Leu	His
		595					600					605			
Glu	Ser	Ala	Lys	Leu	Asn	Val	Glu	Met	Gly	Lys	Ile	His	Ala	Asn	Gln

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610	615	620
Lys Tyr Arg Ala Leu Ile Val Gly Thr Ala Asp Gly Ile Lys Asn Phe		
625	630	635 640
Thr Ser Asp Ala Glu Ala Ile Ala Ala Gly Tyr Val Lys Glu Thr Asp		
	645	650 655
Ser Asn Gly Val Leu Thr Phe Gly Ala Asn Asp Ile Lys Gly Tyr Glu		
	660	665 670
Thr Phe Asp Met Ser Gly Phe Val Ala Val Trp Val Pro Val Gly Ala		
	675	680 685
Ser Asp Asp Gln Asp Ile Arg Val Ala Pro Ser Thr Glu Ala Lys Lys		
	690	695 700
Glu Gly Glu Leu Thr Leu Lys Ala Thr Glu Ala Tyr Asp Ser Gln Leu		
	705	710 715 720
Ile Tyr Glu Gly Phe Ser Asn Phe Gln Thr Ile Pro Asp Gly Ser Asp		
	725	730 735
Pro Ser Val Tyr Thr Asn Arg Lys Ile Ala Glu Asn Val Asp Leu Phe		
	740	745 750
Lys Ser Trp Gly Val Thr Ser Phe Glu Met Ala Pro Gln Phe Val Ser		
	755	760 765
Ala Asp Asp Gly Thr Phe Leu Asp Ser Val Ile Gln Asn Gly Tyr Ala		
	770	775 780
Phe Ala Asp Arg Tyr Asp Leu Ala Met Ser Lys Asn Asn Lys Tyr Gly		
	785	790 795 800
Ser Lys Glu Asp Leu Arg Asp Ala Leu Lys Ala Leu His Lys Ala Gly		
	805	810 815
Ile Gln Ala Ile Ala Asp Trp Val Pro Asp Gln Ile Tyr Gln Leu Pro		
	820	825 830
Gly Lys Glu Val Val Thr Ala Thr Arg Thr Asp Gly Ala Gly Arg Lys		
	835	840 845
Ile Ala Asp Ala Ile Ile Asp His Ser Leu Tyr Val Ala Asn Ser Lys		
	850	855 860
Ser Ser Gly Arg Asp Tyr Gln Ala Gln Tyr Gly Gly Glu Phe Leu Ala		
	865	870 875 880
Glu Leu Lys Ala Lys Tyr Pro Lys Met Phe Thr Glu Asn Met Ile Ser		
	885	890 895
Thr Gly Lys Pro Ile Asp Asp Ser Val Lys Leu Lys Gln Trp Lys Ala		
	900	905 910
Lys Tyr Phe Asn Gly Thr Asn Val Leu Asp Arg Gly Val Gly Tyr Val		
	915	920 925
Leu Ser Asp Glu Ala Thr Gly Lys Tyr Phe Thr Val Thr Lys Glu Gly		
	930	935 940
Asn Phe Ile Pro Leu Gln Leu Thr Gly Asn Glu Lys Ala Val Thr Gly		
	945	950 955 960
Phe Ser Asn Asp Gly Lys Gly Ile Thr Tyr Phe Gly Thr Ser Gly Asn		
	965	970 975
Gln Ala Lys Ser Ala Phe Val Thr Phe Asn Gly Asn Thr Tyr Tyr Phe		
	980	985 990
Asp Ala Arg Gly His Met Val Thr Asn Gly Glu Tyr Ser Pro Asn Gly		
	995	1000 1005
Lys Asp Val Tyr Arg Phe Leu Pro Asn Gly Ile Met Leu Ser Asn		
	1010	1015 1020

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Lys Gly	Gln Met Tyr Lys	Gly Gly Tyr Thr Lys	Phe Asp Val Thr	
1040		1045		1050
Glu Thr	Asp Lys Asp Gly	Asn Glu Ser Lys Val	Val Lys Phe Arg	
1055		1060		1065
Tyr Phe	Thr Asn Glu Gly	Val Met Ala Lys Gly	Leu Thr Val Ile	
1070		1075		1080
Asp Gly	Ser Thr Gln Tyr	Phe Gly Glu Asp Gly	Phe Gln Thr Lys	
1085		1090		1095
Asp Lys	Leu Ala Thr Tyr	Lys Gly Lys Thr Tyr	Tyr Phe Glu Ala	
1100		1105		1110
His Thr	Gly Asn Ala Ile	Lys Asn Thr Trp Arg	Asn Ile Asp Gly	
1115		1120		1125
Lys Trp	Tyr His Phe Asp	Glu Asn Gly Val Ala	Ala Thr Gly Ala	
1130		1135		1140
Gln Val	Ile Asn Gly Gln	Lys Leu Tyr Phe Asn	Glu Asp Gly Ser	
1145		1150		1155
Gln Val	Lys Gly Gly Val	Val Lys Asn Ala Asp	Gly Thr Tyr Ser	
1160		1165		1170
Lys Tyr	Lys Glu Gly Ser	Gly Glu Leu Val Thr	Asn Glu Phe Phe	
1175		1180		1185
Thr Thr	Asp Gly Asn Val	Trp Tyr Tyr Ala Gly	Ala Asp Gly Lys	
1190		1195		1200
Thr Val	Thr Gly Ala Gln	Val Ile Asn Gly Gln	His Leu Tyr Phe	
1205		1210		1215
Lys Glu	Asp Gly Ser Gln	Val Lys Gly Gly Val	Val Lys Asn Ala	
1220		1225		1230
Asp Gly	Thr Tyr Ser Lys	Tyr Asp Ala Ala Thr	Gly Glu Arg Leu	
1235		1240		1245
Thr Asn	Glu Phe Phe Thr	Thr Gly Asp Asn Asn	Trp Tyr Tyr Ile	
1250		1255		1260
Gly Ser	Asn Gly Lys Thr	Val Thr Gly Glu Val	Lys Ile Gly Ala	
1265		1270		1275
Asp Thr	Tyr Tyr Phe Ala	Lys Asp Gly Lys Gln	Val Lys Gly Gln	
1280		1285		1290
Thr Val	Thr Ala Gly Asn	Gly Arg Ile Ser Tyr	Tyr Tyr Gly Asp	
1295		1300		1305
Ser Gly	Lys Lys Ala Ile	Ser Thr Trp Ile Glu	Ile Gln Pro Gly	
1310		1315		1320
Ile Tyr	Val Tyr Phe Asp	Lys Thr Gly Ile Ala	Tyr Pro Pro Arg	
1325		1330		1335
Val Leu Asn				
1340				

<210> SEQ ID NO 31

<400> SEQUENCE: 31

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<210> SEQ ID NO 32

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<400> SEQUENCE: 32

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<210> SEQ ID NO 33

<211> LENGTH: 4026

<212> TYPE: DNA

<213> ORGANISM: *Streptococcus salivarius* JIM8777

<400> SEQUENCE: 33

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gcgtatgaca gcacggaggg atcctttgag ctgatcgatg gttatttgac cgcgatagc	240
tggtatcgtc cggcgagcat cattaaggac ggcgttacgt ggcaggcctc gaccgcagaa	300
gattttcgtc cgctgctgat ggcttggtgg ccgaatgttg acaccaggt gaattatctg	360
aattacatgt ccaaggtttt caacctggat gcaaagtaca ccagcacgga caagcaggaa	420
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<210> SEQ ID NO 34

<211> LENGTH: 1341

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<212> TYPE: PRT

<213> ORGANISM: Streptococcus salivarius JIM8777

<400> SEQUENCE: 34

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Glu Asn Phe Ala Ile Thr Val Asn Gly Gln Leu Leu Tyr Phe Gly Lys
 20           25           30

Asp Gly Ala Leu Thr Ser Ser Ser Thr Tyr Ser Phe Thr Pro Gly Thr
 35           40           45

Thr Asn Ile Val Asp Gly Phe Ser Ile Asn Asn Arg Ala Tyr Asp Ser
 50           55           60

Ser Glu Ala Ser Phe Glu Leu Ile Asp Gly Tyr Leu Thr Ala Asp Ser
 65           70           75           80

Trp Tyr Arg Pro Ala Ser Ile Ile Lys Asp Gly Val Thr Trp Gln Ala
 85           90           95

Ser Thr Ala Glu Asp Phe Arg Pro Leu Leu Met Ala Trp Trp Pro Asn
100          105          110

Val Asp Thr Gln Val Asn Tyr Leu Asn Tyr Met Ser Lys Val Phe Asn
115          120          125

Leu Asp Ala Lys Tyr Thr Ser Thr Asp Lys Gln Glu Thr Leu Asn Val
130          135          140

Ala Ala Lys Asp Ile Gln Val Lys Ile Glu Gln Lys Ile Gln Ala Glu
145          150          155          160

Lys Ser Thr Gln Trp Leu Arg Glu Thr Ile Ser Ala Phe Val Lys Thr
165          170          175

Gln Pro Gln Trp Asn Lys Glu Thr Glu Asn Tyr Ser Lys Gly Gly Gly
180          185          190

Glu Asp His Leu Gln Gly Gly Ala Leu Leu Tyr Val Asn Asp Ser Arg
195          200          205

Thr Pro Trp Ala Asn Ser Asn Tyr Arg Leu Leu Asn His Thr Ala Thr
210          215          220

Asn Gln Lys Gly Thr Ile Asp Lys Ser Val Leu Asp Glu Gln Ser Asp
225          230          235          240

Pro Asn His Met Gly Gly Phe Asp Phe Leu Leu Ala Asn Asp Val Asp
245          250          255

Leu Ser Asn Pro Val Val Gln Ala Glu Gln Leu Asn Gln Ile His Tyr
260          265          270

Leu Met Asn Trp Gly Ser Ile Val Met Gly Asp Lys Asp Ala Asn Phe
275          280          285

Asp Gly Ile Arg Val Asp Ala Val Asp Asn Val Asp Ala Asp Met Leu
290          295          300

Gln Leu Tyr Thr Asn Tyr Phe Arg Glu Tyr Tyr Gly Val Asn Lys Ser
305          310          315          320

Glu Ala Asn Ala Leu Ala His Ile Ser Val Leu Glu Ala Trp Ser Leu
325          330          335

Asn Asp Asn His Tyr Asn Asp Lys Thr Asp Gly Ala Ala Leu Ala Met
340          345          350

Glu Asn Lys Gln Arg Leu Ala Leu Leu Phe Ser Leu Ala Lys Pro Ile
355          360          365

Lys Glu Arg Thr Pro Ala Val Ser Pro Leu Tyr Asn Asn Thr Phe Asn
370          375          380

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Thr	Thr	Gln	Arg	Asp	Glu	Lys	Thr	Asp	Trp	Ile	Asn	Lys	Asp	Gly	Ser	385	390	395	400
Lys	Ala	Tyr	Asn	Glu	Asp	Gly	Thr	Val	Lys	Gln	Ser	Thr	Ile	Gly	Lys	405	410	415	
Tyr	Asn	Glu	Lys	Tyr	Gly	Asp	Ala	Ser	Gly	Asn	Tyr	Val	Phe	Ile	Arg	420	425	430	
Ala	His	Asp	Asn	Asn	Val	Gln	Asp	Ile	Ile	Ala	Glu	Ile	Ile	Lys	Lys	435	440	445	
Glu	Ile	Asn	Pro	Lys	Ser	Asp	Gly	Phe	Thr	Ile	Thr	Asp	Ala	Glu	Met	450	455	460	
Lys	Lys	Ala	Phe	Glu	Ile	Tyr	Asn	Lys	Asp	Met	Leu	Ser	Ser	Asp	Lys	465	470	475	480
Lys	Tyr	Thr	Leu	Asn	Asn	Ile	Pro	Ala	Ala	Tyr	Ala	Val	Met	Leu	Gln	485	490	495	
Asn	Met	Glu	Thr	Ile	Thr	Arg	Val	Tyr	Tyr	Gly	Asp	Leu	Tyr	Thr	Asp	500	505	510	
Asn	Gly	Asn	Tyr	Met	Glu	Thr	Lys	Ser	Pro	Tyr	Tyr	Asp	Thr	Ile	Val	515	520	525	
Asn	Leu	Met	Lys	Asn	Arg	Ile	Lys	Tyr	Val	Ser	Gly	Gly	Gln	Ala	Gln	530	535	540	
Arg	Ser	Tyr	Trp	Leu	Pro	Thr	Asp	Gly	Lys	Met	Asp	Asn	Ser	Asp	Val	545	550	555	560
Glu	Leu	Tyr	Arg	Thr	Asn	Glu	Val	Tyr	Ala	Ser	Val	Arg	Tyr	Gly	Lys	565	570	575	
Asp	Ile	Met	Thr	Ala	Asp	Asp	Thr	Glu	Gly	Ser	Lys	Tyr	Ser	Arg	Thr	580	585	590	
Ser	Gly	Gln	Val	Thr	Leu	Val	Ala	Asn	Asn	Pro	Lys	Leu	Thr	Leu	Asp	595	600	605	
Gln	Ser	Ala	Lys	Leu	Lys	Val	Glu	Met	Gly	Lys	Ile	His	Ala	Asn	Gln	610	615	620	
Lys	Tyr	Arg	Ala	Leu	Ile	Val	Gly	Thr	Ala	Asp	Gly	Ile	Lys	Asn	Phe	625	630	635	640
Thr	Ser	Asp	Ala	Asp	Ala	Ile	Ala	Ala	Gly	Tyr	Val	Lys	Glu	Thr	Asp	645	650	655	
Ser	Asn	Gly	Val	Leu	Thr	Phe	Gly	Ala	Asn	Asp	Ile	Lys	Gly	Tyr	Glu	660	665	670	
Thr	Phe	Asp	Met	Ser	Gly	Phe	Val	Ala	Val	Trp	Val	Pro	Val	Gly	Ala	675	680	685	
Ser	Asp	Asp	Gln	Asp	Ile	Arg	Val	Ala	Pro	Ser	Thr	Glu	Ala	Lys	Lys	690	695	700	
Glu	Gly	Glu	Leu	Thr	Leu	Lys	Ala	Thr	Glu	Ala	Tyr	Asp	Ser	Gln	Leu	705	710	715	720
Ile	Tyr	Glu	Gly	Phe	Ser	Asn	Phe	Gln	Thr	Ile	Pro	Asp	Gly	Ser	Asp	725	730	735	
Pro	Ser	Val	Tyr	Thr	Asn	Arg	Lys	Ile	Ala	Glu	Asn	Val	Asp	Leu	Phe	740	745	750	
Lys	Ser	Trp	Gly	Val	Thr	Ser	Phe	Glu	Met	Ala	Pro	Gln	Phe	Val	Ser	755	760	765	
Ala	Asp	Asp	Gly	Thr	Phe	Leu	Asp	Ser	Val	Ile	Gln	Asn	Gly	Tyr	Ala	770	775	780	

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Phe	Ala	Asp	Arg	Tyr	Asp	Leu	Ala	Met	Ser	Lys	Asn	Asn	Lys	Tyr	Gly	785	790	795	800
Ser	Lys	Glu	Asp	Leu	Arg	Asp	Ala	Leu	Lys	Ala	Leu	His	Lys	Ala	Gly	805	810	815	
Ile	Gln	Ala	Ile	Ala	Asp	Trp	Val	Pro	Asp	Gln	Ile	Tyr	Gln	Leu	Pro	820	825	830	
Gly	Lys	Glu	Val	Val	Thr	Ala	Thr	Arg	Thr	Asp	Gly	Ala	Gly	Arg	Lys	835	840	845	
Ile	Ala	Asp	Ala	Ile	Ile	Asp	His	Ser	Leu	Tyr	Val	Ala	Asn	Thr	Lys	850	855	860	
Ser	Ser	Gly	Lys	Asp	Tyr	Gln	Ala	Lys	Tyr	Gly	Gly	Glu	Phe	Leu	Ala	865	870	875	880
Glu	Leu	Lys	Ala	Lys	Tyr	Pro	Glu	Met	Phe	Lys	Val	Asn	Met	Ile	Ser	885	890	895	
Thr	Gly	Lys	Pro	Ile	Asp	Asp	Ser	Val	Lys	Leu	Lys	Gln	Trp	Lys	Ala	900	905	910	
Glu	Tyr	Phe	Asn	Gly	Thr	Asn	Val	Leu	Glu	Arg	Gly	Val	Gly	Tyr	Val	915	920	925	
Leu	Ser	Asp	Glu	Ala	Thr	Gly	Lys	Tyr	Phe	Thr	Val	Thr	Lys	Asp	Gly	930	935	940	
Asn	Phe	Ile	Pro	Leu	Gln	Leu	Thr	Gly	Asn	Glu	Lys	Val	Val	Thr	Gly	945	950	955	960
Phe	Ser	Asn	Asp	Gly	Lys	Gly	Ile	Thr	Tyr	Phe	Gly	Thr	Ser	Gly	Thr	965	970	975	
Gln	Ala	Lys	Ser	Ala	Phe	Val	Thr	Phe	Asn	Gly	Asn	Thr	Tyr	Tyr	Phe	980	985	990	
Asp	Ala	Arg	Gly	His	Met	Val	Thr	Asn	Gly	Glu	Tyr	Ser	Pro	Asn	Gly	995	1000	1005	
Lys	Asp	Val	Tyr	Arg	Phe	Leu	Pro	Asn	Gly	Ile	Met	Leu	Ser	Asn		1010	1015	1020	
Ala	Phe	Tyr	Val	Asp	Ala	Asn	Gly	Asn	Thr	Tyr	Leu	Tyr	Asn	Ser		1025	1030	1035	
Lys	Gly	Gln	Met	Tyr	Lys	Gly	Gly	Tyr	Thr	Lys	Phe	Asp	Val	Thr		1040	1045	1050	
Glu	Thr	Asp	Lys	Asp	Gly	Lys	Glu	Ser	Lys	Val	Val	Lys	Phe	Arg		1055	1060	1065	
Tyr	Phe	Thr	Asn	Glu	Gly	Val	Met	Ala	Lys	Gly	Val	Thr	Val	Ile		1070	1075	1080	
Asp	Gly	Phe	Thr	Gln	Tyr	Phe	Gly	Glu	Asp	Gly	Phe	Gln	Ala	Lys		1085	1090	1095	
Asp	Lys	Leu	Val	Thr	Phe	Lys	Gly	Lys	Thr	Tyr	Tyr	Phe	Asp	Ala		1100	1105	1110	
His	Thr	Gly	Asn	Ala	Ile	Lys	Asn	Thr	Trp	Arg	Asn	Ile	Asp	Gly		1115	1120	1125	
Lys	Trp	Tyr	His	Phe	Asp	Ala	Asn	Gly	Val	Ala	Ala	Thr	Gly	Ala		1130	1135	1140	
Gln	Val	Ile	Asn	Gly	Gln	Lys	Leu	Tyr	Phe	Asn	Glu	Asp	Gly	Ser		1145	1150	1155	
Gln	Val	Lys	Gly	Gly	Val	Val	Lys	Asn	Ala	Asp	Gly	Thr	Tyr	Ser		1160	1165	1170	
Lys	Tyr	Lys	Glu	Gly	Ser	Gly	Glu	Leu	Val	Thr	Asn	Glu	Phe	Phe					

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1175	1180	1185
Thr Thr Asp Gly Asn Val Trp Tyr Tyr Ala Gly Ala Asn Gly Lys		
1190	1195	1200
Thr Val Thr Gly Ala Gln Val Ile Asn Gly Gln His Leu Tyr Phe		
1205	1210	1215
Asn Ala Asp Gly Ser Gln Val Lys Gly Gly Val Val Lys Asn Ala		
1220	1225	1230
Asp Gly Thr Tyr Ser Lys Tyr Asp Ala Ala Thr Gly Glu Arg Leu		
1235	1240	1245
Thr Asn Glu Phe Phe Thr Thr Gly Asp Asn Asn Trp Tyr Tyr Ile		
1250	1255	1260
Gly Ala Asn Gly Lys Thr Val Thr Gly Glu Val Lys Ile Gly Asp		
1265	1270	1275
Asp Thr Tyr Tyr Phe Ala Lys Asp Gly Lys Gln Val Lys Gly Gln		
1280	1285	1290
Thr Val Ser Ala Gly Asn Gly Arg Ile Ser Tyr Tyr Tyr Gly Asp		
1295	1300	1305
Ser Gly Lys Arg Ala Val Ser Thr Trp Val Glu Ile Gln Pro Gly		
1310	1315	1320
Val Tyr Val Tyr Phe Asp Lys Asn Gly Leu Ala Tyr Pro Pro Arg		
1325	1330	1335
Val Leu Asn		
1340		

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<210> SEQ ID NO 58

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<210> SEQ ID NO 59

<211> LENGTH: 1242

<212> TYPE: PRT

<213> ORGANISM: Streptococcus sp. C150

<400> SEQUENCE: 59

Met Ile Asn Gly Lys Glu Tyr Tyr Val Glu Asp Asp Gly Thr Val Arg
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Lys Asn Tyr Val Leu Glu Arg Asn Gly Gly Ser Gln Tyr Phe Asn Ala
20 25 30

Glu Thr Gly Glu Leu Ser Asn Gln Lys Asp Tyr Arg Phe Asp Lys Asn
35 40 45

Gly Gly Thr Gly Ser Ala Ala Asp Ser Thr Thr Asn Thr Asn Val Thr
50 55 60

Val Asn Gly Asp Lys Asn Ala Phe Tyr Gly Thr Thr Glu Lys Asp Ile
65 70 75 80

Glu Leu Val Asp Gly Tyr Phe Thr Ala Asn Thr Trp Tyr Arg Pro Lys
85 90 95

Glu 100	Ile	Leu	Lys	Asp	Gly	Lys	Glu	Trp	Thr	Ala	Ser	Thr	Glu	Asn	Asp
Lys 115	Arg	Pro	Leu	Leu	Thr	Val	Trp	Trp	Pro	Ser	Lys	Ala	Ile	Gln	Ala
Ser 130	Tyr	Leu	Asn	Tyr	Met	Arg	Glu	Glu	Gly	Leu	Gly	Thr	Asn	Gln	Thr
Phe 145	Thr	Ser	Tyr	Ser	Ser	Gln	Thr	Gln	Met	Asp	Gln	Ala	Ala	Leu	Glu
Val	Gln	Lys	Arg	Ile	Glu	Glu	Arg	Ile	Ala	Arg	Glu	Gly	Asn	Thr	Asp
Trp	Leu	Arg	Thr	Thr	Ile	Lys	Asn	Phe	Val	Lys	Thr	Gln	Pro	Gly	Trp
Asn	Ser	Thr	Ser	Glu	Asn	Leu	Asp	Asn	Ser	Asp	His	Leu	Gln	Gly	Gly
Ala 210	Leu	Leu	Tyr	Asn	Asn	Ser	Asn	Arg	Thr	Ser	Tyr	Ala	Asn	Ser	Asp
Tyr 225	Arg	Leu	Leu	Asn	Arg	Thr	Pro	Thr	Gln	Gln	Asp	Gly	Thr	Arg	Arg
Tyr	Phe	Lys	Asp	Asn	Ser	Ser	Gly	Gly	Phe	Glu	Phe	Leu	Leu	Ala	Asn
Asp	Ile	Asp	Asn	Ser	Asn	Pro	Ala	Val	Gln	Ala	Glu	Gln	Leu	Asn	Trp
Leu	His	Tyr	Ile	Met	Asn	Ile	Gly	Ser	Leu	Thr	Gly	Gly	Ser	Glu	Asp
Glu 290	Asn	Phe	Asp	Gly	Val	Arg	Val	Asp	Ala	Val	Asp	Asn	Val	Asn	Ala
Asp 305	Leu	Leu	Gln	Ile	Ala	Ser	Asp	Tyr	Phe	Lys	Ala	Lys	Tyr	Gly	Val
Glu	Lys	Ser	Glu	Glu	Glu	Ala	Ile	Lys	His	Leu	Ser	Ile	Leu	Glu	Ala
Trp	Ser	His	Asn	Asp	Ala	Tyr	Tyr	Asn	Glu	Asp	Thr	Lys	Gly	Ala	Gln
Leu	Pro	Met	Asp	Asp	Pro	Leu	Arg	Leu	Ala	Met	Val	Phe	Ser	Phe	Leu
Arg 370	Pro	Ile	Gly	Asn	Arg	Ser	Gly	Leu	Glu	Pro	Leu	Ile	Thr	Asn	Ser
Leu 385	Asn	Asp	Arg	Ser	Glu	Ser	Lys	Lys	Asn	Thr	Lys	Arg	Met	Ala	Asn
Tyr	Thr	Phe	Val	Arg	Ala	His	Asp	Ser	Glu	Val	Gln	Ser	Val	Ile	Gly
Gln	Ile	Ile	Lys	Asn	Glu	Ile	Asn	Pro	Gln	Ser	Thr	Gly	Asn	Thr	Phe
Thr	Leu	Asp	Glu	Met	Lys	Lys	Ala	Phe	Lys	Ile	Tyr	Asn	Ala	Asp	Met
Arg 450	Ser	Ala	Asn	Lys	Arg	Tyr	Thr	Gln	Tyr	Asn	Ile	Pro	Ser	Ala	Tyr
Ala 465	Phe	Met	Leu	Thr	Asn	Lys	Asp	Thr	Val	Pro	Arg	Val	Tyr	Tyr	Gly
Asp	Leu	Tyr	Thr	Asp	Asp	Gly	Gln	Tyr	Met	Ala	Gln	Lys	Ser	Pro	Tyr

His 500	Asp	Ala	Ile	Ser	Thr	Leu	Leu	Gln	Ala	Arg	Ile	Arg	Tyr	Ala
Gly	Gly	Gln	Asp	Met	Lys	Met	Ser	Tyr	Val	Gly	Ser	Gly	Asn	Thr
Gly	Trp	Asp	Ala	Ser	Gly	Val	Leu	Thr	Ser	Val	Arg	Tyr	Gly	Lys
Ala 545	Asn	Asn	Ala	Ser	Asp	Ala	Gly	Thr	Ala	Glu	Thr	Arg	Asn	Gln
Met	Ala	Val	Ile	Leu	Ser	Asn	Gln	Pro	Ala	Leu	Arg	Leu	Asn	Ser
Leu	Thr	Ile	Asn	Met	Gly	Ala	Ala	His	Arg	Asn	Gln	Ala	Tyr	Arg
Leu	Leu	Leu	Thr	Thr	Ser	Asn	Gly	Val	Ala	Ser	Tyr	Leu	Asn	Asp
Asp	Ala	Asn	Gly	Ile	Val	Lys	Tyr	Thr	Asp	Ala	Asn	Gly	Tyr	Leu
Phe 625	Asn	Pro	Gly	Glu	Ile	Ser	Gly	Val	Arg	Asn	Ala	Gln	Val	Asp
Tyr	Leu	Ala	Val	Trp	Val	Pro	Leu	Gly	Ala	Ser	Glu	Asn	Gln	Asp
Arg	Val	Ala	Ala	Ser	Lys	Ser	Lys	Asn	Ser	Ser	Gly	Leu	Val	Tyr
Ser	Ser	Ala	Ala	Leu	Asp	Ser	Gln	Val	Ile	Tyr	Glu	Gly	Phe	Ser
Phe 690	Gln	Asp	Phe	Val	Gln	Asp	Pro	Ser	Gln	Tyr	Thr	Asn	Lys	Lys
Ala 705	Glu	Asn	Ala	Asn	Leu	Phe	Lys	Ser	Trp	Gly	Ile	Thr	Ser	Phe
Phe	Ala	Pro	Gln	Tyr	Val	Ser	Ser	Asp	Asp	Gly	Thr	Phe	Leu	Asp
Val	Ile	Gln	Asn	Gly	Tyr	Ala	Phe	Ser	Asp	Arg	Tyr	Asp	Ile	Gly
Ser	Lys	Asp	Asn	Lys	Tyr	Gly	Ser	Leu	Ala	Asp	Leu	Lys	Ala	Ala
Lys 770	Ser	Leu	His	Ala	Val	Gly	Ile	Ser	Ala	Ile	Ala	Asp	Trp	Val
Asp 785	Gln	Ile	Tyr	Asn	Leu	Pro	Gly	Asp	Glu	Val	Val	Thr	Ala	Thr
Val	Asn	Asn	Tyr	Gly	Glu	Thr	Lys	Asp	Gly	Ala	Ile	Ile	Asp	His
Leu	Tyr	Val	Ala	Lys	Thr	Arg	Thr	Phe	Gly	Asn	Asp	Tyr	Gln	Gly
Tyr	Gly	Gly	Ala	Tyr	Leu	Asp	Glu	Leu	Lys	Arg	Leu	Tyr	Pro	Gln
Phe 850	Asp	Arg	Val	Gln	Ile	Ser	Thr	Gly	Lys	Arg	Leu	Thr	Thr	Asp
Lys 865	Ile	Thr	Lys	Trp	Ser	Ala	Lys	Tyr	Met	Asn	Gly	Thr	Asn	Ile
Asp	Arg	Gly	Ser	Glu	Tyr	Val	Leu	Lys	Asn	Gly	Leu	Ser	Gly	Tyr
Gly	Thr	Asn	Gly	Gly	Lys	Val	Ser	Leu	Pro	Lys	Val	Val	Gly	Ser

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900				905				910							
Gln	Ser	Thr	Asn	Asn	Asn	Asn	Gln	Asn	Gly	Asp	Gly	Ser	Gly	Arg	Phe
	915						920						925		
Glu	Lys	Ser	Trp	Gly	Ser	Val	Tyr	Tyr	Arg	Tyr	Asn	Asp	Gly	Gln	Arg
	930					935					940				
Ala	Arg	Asn	Ala	Phe	Ile	Lys	Asp	Asn	Asp	Gly	Asn	Val	Tyr	Tyr	Phe
	945				950					955					960
Asp	Asn	Thr	Gly	Arg	Met	Ala	Ile	Gly	Glu	Lys	Thr	Ile	Asp	Gly	Lys
				965						970				975	
Gln	Tyr	Phe	Phe	Leu	Ala	Asn	Gly	Val	Gln	Leu	Arg	Asp	Gly	Tyr	Arg
			980							985				990	
Gln	Asn	Arg	Arg	Gly	Gln	Val	Phe	Tyr	Tyr	Asp	Glu	Asn	Gly	Ile	Met
		995					1000						1005		
Ser	Gln	Thr	Gly	Lys	Pro	Ser	Pro	Lys	Pro	Glu	Pro	Lys	Pro	Asp	
	1010					1015							1020		
Asn	Asn	Thr	Phe	Ser	Arg	Asn	Gln	Phe	Ile	Gln	Ile	Gly	Asn	Asn	
	1025					1030							1035		
Val	Trp	Ala	Tyr	Tyr	Asp	Gly	Asn	Gly	Lys	Arg	Val	Ile	Gly	Arg	
	1040					1045							1050		
Gln	Asn	Ile	Asn	Gly	Gln	Glu	Leu	Phe	Phe	Asp	Asn	Asn	Gly	Val	
	1055					1060							1065		
Gln	Val	Lys	Gly	Arg	Thr	Ala	Gln	Val	Asp	Gly	Val	Thr	Arg	Tyr	
	1070					1075							1080		
Phe	Asp	Ala	Asn	Ser	Gly	Glu	Met	Ala	Arg	Asn	Arg	Phe	Ala	Glu	
	1085					1090							1095		
Val	Glu	Pro	Gly	Val	Trp	Ala	Tyr	Phe	Asn	Asn	Asp	Gly	Ala	Ala	
	1100					1105							1110		
Val	Thr	Gly	Ser	Gln	Asn	Ile	Asn	Gly	Gln	Thr	Leu	Tyr	Phe	Asp	
	1115					1120							1125		
Gln	Asn	Gly	His	Gln	Val	Lys	Gly	Ala	Leu	Val	Thr	Val	Asp	Gly	
	1130					1135							1140		
Asn	Leu	Arg	Tyr	Tyr	Asp	Ala	Asn	Ser	Gly	Asp	Leu	Tyr	Arg	Asn	
	1145					1150							1155		
Arg	Phe	Gln	Glu	Val	Asn	Gly	Ser	Trp	Tyr	Tyr	Phe	Asp	Gly	Asn	
	1160					1165							1170		
Gly	Asn	Ala	Val	Lys	Gly	Met	Val	Asn	Ile	Asn	Gly	Gln	Asn	Leu	
	1175					1180							1185		
Leu	Phe	Asp	Asn	Asp	Gly	Lys	Gln	Val	Lys	Gly	His	Leu	Val	Arg	
	1190					1195							1200		
Val	Asn	Gly	Val	Ile	Arg	Tyr	Tyr	Asp	Pro	Asn	Ser	Gly	Glu	Met	
	1205					1210							1215		
Ala	Val	Asn	Arg	Trp	Val	Glu	Ile	Ser	Ser	Gly	Trp	Trp	Val	Tyr	
	1220					1225							1230		
Phe	Asp	Gly	Glu	Gly	Arg	Gly	Gln	Ile							
	1235					1240									

<210> SEQ ID NO 60

<211> LENGTH: 1518

<212> TYPE: PRT

<213> ORGANISM: Streptococcus salivarius

<400> SEQUENCE: 60

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Met	Glu	Asn	Lys	Ile	His	Tyr	Lys	Leu	His	Lys	Val	Lys	Lys	Gln	Trp	1	5	10	15
Val	Thr	Ile	Ala	Val	Ala	Ser	Val	Ala	Leu	Ala	Thr	Val	Leu	Gly	Gly	20	25	30	
Leu	Ser	Val	Thr	Thr	Ser	Ser	Val	Ser	Ala	Asp	Glu	Thr	Gln	Asp	Lys	35	40	45	
Thr	Val	Thr	Gln	Ser	Asn	Ser	Gly	Thr	Thr	Ala	Ser	Leu	Val	Thr	Ser	50	55	60	
Pro	Glu	Ala	Thr	Lys	Glu	Ala	Asp	Lys	Arg	Thr	Asn	Thr	Lys	Glu	Ala	65	70	75	80
Asp	Val	Leu	Thr	Pro	Ala	Lys	Glu	Thr	Asn	Ala	Val	Glu	Thr	Ala	Thr	85	90	95	
Thr	Thr	Asn	Thr	Gln	Ala	Thr	Ala	Glu	Ala	Ala	Thr	Thr	Ala	Thr	Thr	100	105	110	
Ala	Asp	Val	Ala	Val	Ala	Ala	Val	Pro	Asn	Lys	Glu	Ala	Val	Val	Thr	115	120	125	
Thr	Asp	Ala	Pro	Ala	Val	Thr	Thr	Glu	Lys	Ala	Glu	Glu	Gln	Pro	Ala	130	135	140	
Thr	Val	Lys	Ala	Glu	Val	Val	Asn	Thr	Glu	Val	Lys	Ala	Pro	Glu	Ala	145	150	155	160
Ala	Leu	Lys	Asp	Ser	Glu	Val	Glu	Ala	Ala	Leu	Ser	Leu	Lys	Asn	Ile	165	170	175	
Lys	Asn	Ile	Asp	Gly	Lys	Tyr	Tyr	Tyr	Val	Asn	Glu	Asp	Gly	Ser	His	180	185	190	
Lys	Glu	Asn	Phe	Ala	Ile	Thr	Val	Asn	Gly	Gln	Leu	Leu	Tyr	Phe	Gly	195	200	205	
Lys	Asp	Gly	Ala	Leu	Thr	Ser	Ser	Ser	Thr	Tyr	Ser	Phe	Thr	Pro	Gly	210	215	220	
Thr	Thr	Asn	Ile	Val	Asp	Gly	Phe	Ser	Ile	Asn	Asn	Arg	Ala	Tyr	Asp	225	230	235	240
Ser	Ser	Glu	Ala	Ser	Phe	Glu	Leu	Ile	Asp	Gly	Tyr	Leu	Thr	Ala	Asp	245	250	255	
Ser	Trp	Tyr	Arg	Pro	Ala	Ser	Ile	Ile	Lys	Asp	Gly	Val	Thr	Trp	Gln	260	265	270	
Ala	Ser	Thr	Ala	Glu	Asp	Phe	Arg	Pro	Leu	Leu	Met	Ala	Trp	Trp	Pro	275	280	285	
Asn	Val	Asp	Thr	Gln	Val	Asn	Tyr	Leu	Asn	Tyr	Met	Ser	Lys	Val	Phe	290	295	300	
Asn	Leu	Asp	Ala	Lys	Tyr	Ser	Ser	Thr	Asp	Lys	Gln	Glu	Thr	Leu	Lys	305	310	315	320
Val	Ala	Ala	Lys	Asp	Ile	Gln	Ile	Lys	Ile	Glu	Gln	Lys	Ile	Gln	Ala	325	330	335	
Glu	Lys	Ser	Thr	Gln	Trp	Leu	Arg	Glu	Thr	Ile	Ser	Ala	Phe	Val	Lys	340	345	350	
Thr	Gln	Pro	Gln	Trp	Asn	Lys	Glu	Thr	Glu	Asn	Tyr	Ser	Lys	Gly	Gly	355	360	365	
Gly	Glu	Asp	His	Leu	Gln	Gly	Gly	Ala	Leu	Leu	Tyr	Val	Asn	Asp	Ser	370	375	380	
Arg	Thr	Pro	Trp	Ala	Asn	Ser	Asp	Tyr	Arg	Arg	Leu	Asn	Arg	Thr	Ala	385	390	395	400
Thr	Asn	Gln	Thr	Gly	Thr	Ile	Asp	Lys	Ser	Ile	Leu	Asp	Glu	Gln	Ser				

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405								410					415				
Asp	Pro	Asn	His	Met	Gly	Gly	Phe	Asp	Phe	Leu	Leu	Ala	Asn	Asp	Val		
			420				425						430				
Asp	Leu	Ser	Asn	Pro	Val	Val	Gln	Ala	Glu	Gln	Leu	Asn	Gln	Ile	His		
			435				440						445				
Tyr	Leu	Met	Asn	Trp	Gly	Ser	Ile	Val	Met	Gly	Asp	Lys	Asp	Ala	Asn		
			450				455						460				
Phe	Asp	Gly	Ile	Arg	Val	Asp	Ala	Val	Asp	Asn	Val	Asp	Ala	Asp	Met		
			465				470						475				
Leu	Gln	Leu	Tyr	Thr	Asn	Tyr	Phe	Arg	Glu	Tyr	Tyr	Gly	Val	Asn	Lys		
			485				490						495				
Ser	Glu	Ala	Asn	Ala	Leu	Ala	His	Ile	Ser	Val	Leu	Glu	Ala	Trp	Ser		
			500				505						510				
Leu	Asn	Asp	Asn	His	Tyr	Asn	Asp	Lys	Thr	Asp	Gly	Ala	Ala	Leu	Ala		
			515				520						525				
Met	Glu	Asn	Lys	Gln	Arg	Leu	Ala	Leu	Leu	Phe	Ser	Leu	Ala	Lys	Pro		
			530				535						540				
Ile	Lys	Glu	Arg	Thr	Pro	Ala	Val	Ser	Pro	Leu	Tyr	Asn	Asn	Thr	Phe		
			545				550						555				
Asn	Thr	Thr	Gln	Arg	Asp	Glu	Lys	Thr	Asp	Trp	Ile	Asn	Lys	Asp	Gly		
			565				570						575				
Ser	Lys	Ala	Tyr	Asn	Glu	Asp	Gly	Thr	Val	Lys	Gln	Ser	Thr	Ile	Gly		
			580				585						590				
Lys	Tyr	Asn	Glu	Lys	Tyr	Gly	Asp	Ala	Ser	Gly	Asn	Tyr	Val	Phe	Ile		
			595				600						605				
Arg	Ala	His	Asp	Asn	Asn	Val	Gln	Asp	Ile	Ile	Ala	Glu	Ile	Ile	Lys		
			610				615						620				
Lys	Glu	Ile	Asn	Pro	Lys	Ser	Asp	Gly	Phe	Thr	Ile	Thr	Asp	Ala	Glu		
			625				630						635				
Met	Lys	Gln	Ala	Phe	Glu	Ile	Tyr	Asn	Lys	Asp	Met	Leu	Ser	Ser	Asp		
			645				650						655				
Lys	Lys	Tyr	Thr	Leu	Asn	Asn	Ile	Pro	Ala	Ala	Tyr	Ala	Val	Met	Leu		
			660				665						670				
Gln	Asn	Met	Glu	Thr	Ile	Thr	Arg	Val	Tyr	Tyr	Gly	Asp	Leu	Tyr	Thr		
			675				680						685				
Asp	Asp	Gly	His	Tyr	Met	Glu	Thr	Lys	Ser	Pro	Tyr	Tyr	Asp	Thr	Ile		
			690				695						700				
Val	Asn	Leu	Met	Lys	Ser	Arg	Ile	Lys	Tyr	Val	Ser	Gly	Gly	Gln	Ala		
			705				710						715				
Gln	Arg	Ser	Tyr	Trp	Leu	Pro	Thr	Asp	Gly	Lys	Met	Asp	Asn	Ser	Asp		
			725				730						735				
Val	Glu	Leu	Tyr	Arg	Thr	Asn	Glu	Val	Tyr	Thr	Ser	Val	Arg	Tyr	Gly		
			740				745						750				
Lys	Asp	Ile	Met	Thr	Ala	Asn	Asp	Thr	Glu	Gly	Ser	Lys	Tyr	Ser	Arg		
			755				760						765				
Thr	Ser	Gly	Gln	Val	Thr	Leu	Val	Ala	Asn	Asn	Pro	Lys	Leu	Asn	Leu		
			770				775						780				
Asp	Gln	Ser	Ala	Lys	Leu	Asn	Val	Glu	Met	Gly	Lys	Ile	His	Ala	Asn		
			785				790						795				
Gln	Lys	Tyr	Arg	Ala	Leu	Ile	Val	Gly	Thr	Ala	Asp	Gly	Ile	Lys	Asn		
			805				810						815				

Phe 820	Thr	Ser	Asp	Ala	Asp	Ala	Ile	Ala	Ala	Gly	Tyr	Val	Lys	Glu	Thr
Asp 835	Ser	Asn	Gly	Val	Leu	Thr	Phe	Gly	Ala	Asn	Asp	Ile	Lys	Gly	Tyr
Glu 850	Thr	Phe	Asp	Met	Ser	Gly	Phe	Val	Ala	Val	Trp	Val	Pro	Val	Gly
Ala 865	Ser	Asp	Asn	Gln	Asp	Ile	Arg	Val	Ala	Pro	Ser	Thr	Glu	Ala	Lys
Lys	Glu	Gly	Glu	Leu	Thr	Leu	Lys	Ala	Thr	Glu	Ala	Tyr	Asp	Ser	Gln
Leu	Ile	Tyr	Glu	Gly	Phe	Ser	Asn	Phe	Gln	Thr	Ile	Pro	Asp	Gly	Ser
Asp	Pro	Ser	Val	Tyr	Thr	Asn	Arg	Lys	Ile	Ala	Glu	Asn	Val	Asp	Leu
Phe 930	Lys	Ser	Trp	Gly	Val	Thr	Ser	Phe	Glu	Met	Ala	Pro	Gln	Phe	Val
Ser 945	Ala	Asp	Asp	Gly	Thr	Phe	Leu	Asp	Ser	Val	Ile	Gln	Asn	Gly	Tyr
Ala	Phe	Ala	Asp	Arg	Tyr	Asp	Leu	Ala	Met	Ser	Lys	Asn	Asn	Lys	Tyr
Gly	Ser	Lys	Glu	Asp	Leu	Arg	Asp	Ala	Leu	Lys	Ala	Leu	His	Lys	Ala
Gly 995	Ile	Gln	Ala	Ile	Ala	Asp	Trp	Val	Pro	Asp	Gln	Ile	Tyr	Gln	Leu
Pro 1010	Gly	Lys	Glu	Val	Val	Thr	Ala	Thr	Arg	Thr	Asp	Gly	Ala	Gly	
Arg 1025	Lys	Ile	Ala	Asp	Ala	Ile	Ile	Asp	His	Ser	Leu	Tyr	Val	Ala	
Asn 1040	Ser	Lys	Ser	Ser	Gly	Lys	Asp	Tyr	Gln	Ala	Lys	Tyr	Gly	Gly	
Glu 1055	Phe	Leu	Ala	Glu	Leu	Lys	Ala	Lys	Tyr	Pro	Glu	Met	Phe	Lys	
Val 1070	Asn	Met	Ile	Ser	Thr	Gly	Lys	Pro	Ile	Asp	Asp	Ser	Val	Lys	
Leu 1085	Lys	Gln	Trp	Lys	Ala	Glu	Tyr	Phe	Asn	Gly	Thr	Asn	Val	Leu	
Glu 1100	Arg	Gly	Val	Gly	Tyr	Val	Leu	Ser	Asp	Glu	Ala	Thr	Gly	Lys	
Tyr 1115	Phe	Thr	Val	Thr	Lys	Glu	Gly	Asn	Phe	Ile	Pro	Leu	Gln	Leu	
Thr 1130	Gly	Lys	Glu	Lys	Val	Ile	Thr	Gly	Phe	Ser	Ser	Asp	Gly	Lys	
Gly 1145	Ile	Thr	Tyr	Phe	Gly	Thr	Ser	Gly	Thr	Gln	Ala	Lys	Ser	Ala	
Phe 1160	Val	Thr	Phe	Asn	Gly	Asn	Thr	Tyr	Tyr	Phe	Asp	Ala	Arg	Gly	
His 1175	Met	Val	Thr	Asn	Ser	Glu	Tyr	Ser	Pro	Asn	Gly	Lys	Asp	Val	
Tyr 1190	Arg	Phe	Leu	Pro	Asn	Gly	Ile	Met	Leu	Ser	Asn	Ala	Phe	Tyr	

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Ile	Asp	Ala	Asn	Gly	Asn	Thr	Tyr	Leu	Tyr	Asn	Ser	Lys	Gly	Gln
1205						1210					1215			
Met	Tyr	Lys	Gly	Gly	Tyr	Thr	Lys	Phe	Asp	Val	Ser	Glu	Thr	Asp
1220						1225					1230			
Lys	Asp	Gly	Lys	Glu	Ser	Lys	Val	Val	Lys	Phe	Arg	Tyr	Phe	Thr
1235						1240					1245			
Asn	Glu	Gly	Val	Met	Ala	Lys	Gly	Val	Thr	Val	Ile	Asp	Gly	Phe
1250						1255					1260			
Thr	Gln	Tyr	Phe	Gly	Glu	Asp	Gly	Phe	Gln	Ala	Lys	Asp	Lys	Leu
1265						1270					1275			
Val	Thr	Phe	Lys	Gly	Lys	Thr	Tyr	Tyr	Phe	Asp	Ala	His	Thr	Gly
1280						1285					1290			
Asn	Gly	Ile	Lys	Asp	Thr	Trp	Arg	Asn	Ile	Asn	Gly	Lys	Trp	Tyr
1295						1300					1305			
Tyr	Phe	Asp	Ala	Asn	Gly	Val	Ala	Ala	Thr	Gly	Ala	Gln	Val	Ile
1310						1315					1320			
Asn	Gly	Gln	Lys	Leu	Tyr	Phe	Asn	Glu	Asp	Gly	Ser	Gln	Val	Lys
1325						1330					1335			
Gly	Gly	Val	Val	Lys	Asn	Ala	Asp	Gly	Thr	Tyr	Ser	Lys	Tyr	Lys
1340						1345					1350			
Glu	Gly	Phe	Gly	Glu	Leu	Val	Thr	Asn	Glu	Phe	Phe	Thr	Thr	Asp
1355						1360					1365			
Gly	Asn	Val	Trp	Tyr	Tyr	Ala	Gly	Ala	Asn	Gly	Lys	Thr	Val	Thr
1370						1375					1380			
Gly	Ala	Gln	Val	Ile	Asn	Gly	Gln	His	Leu	Tyr	Phe	Asn	Ala	Asp
1385						1390					1395			
Gly	Ser	Gln	Val	Lys	Gly	Gly	Val	Val	Lys	Asn	Ala	Asp	Gly	Thr
1400						1405					1410			
Tyr	Ser	Lys	Tyr	Asn	Ala	Ser	Thr	Gly	Glu	Arg	Leu	Thr	Asn	Glu
1415						1420					1425			
Phe	Phe	Thr	Thr	Gly	Asp	Asn	Asn	Trp	Tyr	Tyr	Ile	Gly	Ala	Asn
1430						1435					1440			
Gly	Lys	Ser	Val	Thr	Gly	Glu	Val	Lys	Ile	Gly	Asp	Asp	Thr	Tyr
1445						1450					1455			
Phe	Phe	Ala	Lys	Asp	Gly	Lys	Gln	Val	Lys	Gly	Gln	Thr	Val	Ser
1460						1465					1470			
Ala	Gly	Asn	Gly	Arg	Ile	Ser	Tyr	Tyr	Tyr	Gly	Asp	Ser	Gly	Lys
1475						1480					1485			
Arg	Ala	Val	Ser	Thr	Trp	Ile	Glu	Ile	Gln	Pro	Gly	Val	Tyr	Val
1490						1495					1500			
Tyr	Phe	Asp	Lys	Asn	Gly	Leu	Ala	Tyr	Pro	Pro	Arg	Val	Leu	Asn
1505						1510					1515			

<210> SEQ ID NO 61

<211> LENGTH: 1528

<212> TYPE: PRT

<213> ORGANISM: Streptococcus salivarius K12

<400> SEQUENCE: 61

Met	Thr	Asn	Lys	Ile	Thr	Gly	Lys	Ile	Ile	Met	Glu	Asn	Lys	Val	His
1						5				10				15	

Tyr	Lys	Leu	His	Lys	Val	Lys	Lys	Gln	Trp	Val	Thr	Ile	Ala	Val	Ala
					20				25					30	

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Ser	Ala	Ala	Leu	Ala	Thr	Val	Val	Gly	Gly	Leu	Ser	Ala	Thr	Thr	Ser	
	35						40					45				
Ser	Val	Ser	Ala	Asp	Glu	Thr	Gln	Asp	Lys	Ile	Val	Thr	Gln	Pro	Asn	
	50					55					60					
Leu	Asp	Thr	Thr	Ala	Asp	Leu	Val	Thr	Ser	Thr	Glu	Ala	Thr	Lys	Glu	
65					70					75					80	
Val	Asp	Lys	Arg	Thr	Asn	Thr	Lys	Glu	Ala	Asp	Val	Leu	Thr	Pro	Ala	
			85						90					95		
Lys	Glu	Thr	Asn	Ala	Val	Glu	Thr	Ala	Thr	Thr	Thr	Asn	Thr	Gln	Ala	
			100					105					110			
Thr	Ala	Glu	Ala	Ala	Thr	Thr	Ala	Thr	Thr	Ser	Asp	Val	Ala	Val	Ala	
	115						120					125				
Ala	Val	Pro	Asn	Lys	Glu	Ala	Val	Val	Thr	Thr	Asp	Ala	Pro	Ala	Val	
	130					135					140					
Thr	Thr	Glu	Lys	Ala	Glu	Glu	Gln	Pro	Ala	Thr	Val	Lys	Ala	Glu	Val	
145					150					155					160	
Val	Asn	Thr	Glu	Val	Lys	Ala	Pro	Gln	Ala	Ala	Leu	Lys	Asp	Ser	Glu	
			165					170						175		
Val	Glu	Ala	Ala	Leu	Ser	Leu	Lys	Asn	Ile	Lys	Tyr	Thr	Asp	Gly	Lys	
		180						185					190			
Tyr	Tyr	Tyr	Val	Asn	Glu	Asp	Gly	Ser	His	Lys	Glu	Asn	Phe	Ala	Ile	
	195						200					205				
Thr	Val	Asn	Gly	Gln	Leu	Leu	Tyr	Phe	Gly	Lys	Asp	Gly	Ala	Leu	Thr	
	210					215					220					
Ser	Ser	Ser	Thr	His	Ser	Phe	Thr	Pro	Gly	Thr	Thr	Asn	Ile	Val	Asp	
225					230					235				240		
Gly	Phe	Ser	Ile	Asn	Asn	Arg	Ala	Tyr	Asp	Ser	Ser	Glu	Ala	Ser	Phe	
			245						250					255		
Glu	Leu	Ile	Asn	Gly	Tyr	Leu	Thr	Ala	Asp	Ser	Trp	Tyr	Arg	Pro	Val	
		260						265					270			
Ser	Ile	Ile	Lys	Asp	Gly	Val	Thr	Trp	Gln	Ala	Ser	Thr	Ala	Glu	Asp	
	275						280					285				
Phe	Arg	Pro	Leu	Leu	Met	Ala	Trp	Trp	Pro	Asn	Val	Asp	Thr	Gln	Val	
	290					295					300					
Asn	Tyr	Leu	Asn	Tyr	Met	Ser	Lys	Val	Phe	Asn	Leu	Glu	Ala	Lys	Tyr	
305				310						315					320	
Thr	Ser	Thr	Asp	Lys	Gln	Ala	Asp	Leu	Asn	Arg	Ala	Ala	Lys	Asp	Ile	
			325					330						335		
Gln	Val	Lys	Ile	Glu	Gln	Lys	Ile	Gln	Ala	Glu	Lys	Ser	Thr	Gln	Trp	
		340						345					350			
Leu	Arg	Glu	Thr	Ile	Ser	Ala	Phe	Val	Lys	Thr	Gln	Pro	Gln	Trp	Asn	
	355						360					365				
Lys	Glu	Thr	Glu	Asn	Tyr	Ser	Lys	Gly	Gly	Gly	Glu	Asp	His	Leu	Gln	
	370					375					380					
Gly	Gly	Ala	Leu	Leu	Tyr	Val	Asn	Asp	Ser	Arg	Thr	Pro	Trp	Ala	Asn	
385					390					395					400	
Ser	Asn	Tyr	Arg	Leu	Leu	Asn	Arg	Thr	Ala	Thr	Asn	Gln	Thr	Gly	Thr	
			405					410						415		
Ile	Asn	Lys	Ser	Val	Leu	Asp	Glu	Gln	Ser	Asp	Pro	Asn	His	Met	Gly	
			420					425					430			

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Gly	Phe	Asp	Phe	Leu	Leu	Ala	Asn	Asp	Val	Asp	Leu	Ser	Asn	Pro	Val
		435					440					445			
Val	Gln	Ala	Glu	Gln	Leu	Asn	Gln	Ile	His	Tyr	Leu	Met	Asn	Trp	Gly
	450					455					460				
Ser	Ile	Val	Met	Gly	Asp	Lys	Asp	Ala	Asn	Phe	Asp	Gly	Ile	Arg	Val
465					470					475					480
Asp	Ala	Val	Asp	Asn	Val	Asn	Ala	Asp	Met	Leu	Gln	Leu	Tyr	Thr	Asn
				485					490					495	
Tyr	Phe	Arg	Glu	Tyr	Tyr	Gly	Val	Asn	Lys	Ser	Glu	Ala	Gln	Ala	Leu
			500					505					510		
Ala	His	Ile	Ser	Val	Leu	Glu	Ala	Trp	Ser	Leu	Asn	Asp	Asn	His	Tyr
		515					520					525			
Asn	Asp	Lys	Thr	Asp	Gly	Ala	Ala	Leu	Ala	Met	Glu	Asn	Lys	Gln	Arg
	530					535					540				
Leu	Ala	Leu	Leu	Phe	Ser	Leu	Ala	Lys	Pro	Ile	Lys	Asp	Arg	Thr	Pro
545					550					555					560
Ala	Val	Ser	Pro	Leu	Tyr	Asn	Asn	Thr	Phe	Asn	Thr	Thr	Gln	Arg	Asp
				565					570					575	
Phe	Lys	Thr	Asp	Trp	Ile	Asn	Lys	Asp	Gly	Ser	Thr	Ala	Tyr	Asn	Glu
			580					585					590		
Asp	Gly	Thr	Ala	Lys	Gln	Ser	Thr	Ile	Gly	Lys	Tyr	Asn	Glu	Lys	Tyr
		595					600					605			
Gly	Asp	Ala	Ser	Gly	Asn	Tyr	Val	Phe	Ile	Arg	Ala	His	Asp	Asn	Asn
	610					615					620				
Val	Gln	Asp	Ile	Ile	Ala	Glu	Ile	Ile	Lys	Lys	Glu	Ile	Asn	Lys	Lys
625					630					635					640
Ser	Asp	Gly	Phe	Thr	Ile	Ser	Asp	Ser	Glu	Met	Lys	Gln	Ala	Phe	Glu
				645					650					655	
Ile	Tyr	Asn	Lys	Asp	Met	Leu	Ser	Ser	Asn	Lys	Lys	Tyr	Thr	Leu	Asn
		660						665					670		
Asn	Ile	Pro	Ala	Ala	Tyr	Ala	Val	Met	Leu	Gln	Asn	Met	Glu	Thr	Ile
		675					680					685			
Thr	Arg	Val	Tyr	Tyr	Gly	Asp	Leu	Tyr	Thr	Asp	Asp	Gly	His	Tyr	Met
	690					695					700				
Glu	Thr	Lys	Ser	Pro	Tyr	His	Asp	Thr	Ile	Val	Asn	Leu	Met	Lys	Asn
705					710					715					720
Arg	Ile	Lys	Tyr	Val	Ser	Gly	Gly	Gln	Ala	Gln	Arg	Ser	Tyr	Trp	Leu
				725					730					735	
Pro	Thr	Asp	Gly	Lys	Met	Asp	Asn	Ser	Asp	Val	Glu	Leu	Tyr	Arg	Thr
			740					745					750		
Ser	Glu	Val	Tyr	Thr	Ser	Val	Arg	Tyr	Gly	Lys	Asp	Ile	Met	Thr	Ala
		755					760					765			
Asp	Asp	Thr	Glu	Gly	Ser	Lys	Tyr	Ser	Arg	Thr	Ser	Gly	Gln	Val	Thr
	770					775						780			
Leu	Val	Val	Asn	Asn	Pro	Lys	Leu	Thr	Leu	His	Glu	Ser	Ala	Lys	Leu
785					790					795					800
Asn	Val	Glu	Met	Gly	Lys	Ile	His	Ala	Asn	Gln	Lys	Tyr	Arg	Ala	Leu
				805					810					815	
Ile	Val	Gly	Thr	Ala	Asp	Gly	Ile	Lys	Asn	Phe	Thr	Ser	Asp	Ala	Glu
			820					825					830		
Ala	Ile	Ala	Ala	Gly	Tyr	Val	Lys	Glu	Thr	Asp	Ser	Asn	Gly	Val	Leu

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835					840					845					
Thr	Phe	Gly	Ala	Asn	Asp	Ile	Lys	Gly	Tyr	Glu	Thr	Phe	Asp	Met	Ser
850						855					860				
Gly	Phe	Val	Ala	Val	Trp	Val	Pro	Val	Gly	Ala	Ser	Asp	Asp	Gln	Asp
865					870					875				880	
Ile	Arg	Val	Ala	Pro	Ser	Thr	Glu	Ala	Lys	Lys	Glu	Gly	Glu	Leu	Thr
				885					890					895	
Leu	Lys	Ala	Thr	Glu	Ala	Tyr	Asp	Ser	Gln	Leu	Ile	Tyr	Glu	Gly	Phe
			900					905					910		
Ser	Asn	Phe	Gln	Thr	Ile	Pro	Asp	Gly	Ser	Asp	Pro	Ser	Val	Tyr	Thr
	915						920					925			
Asn	Arg	Lys	Ile	Ala	Glu	Asn	Val	Asp	Leu	Phe	Lys	Ser	Trp	Gly	Val
930						935					940				
Thr	Ser	Phe	Glu	Met	Ala	Pro	Gln	Phe	Val	Ser	Ala	Asp	Asp	Gly	Thr
945				950					955					960	
Phe	Leu	Asp	Ser	Val	Ile	Gln	Asn	Gly	Tyr	Ala	Phe	Ala	Asp	Arg	Tyr
			965					970						975	
Asp	Leu	Ala	Met	Ser	Lys	Asn	Asn	Lys	Tyr	Gly	Ser	Lys	Glu	Asp	Leu
		980						985					990		
Arg	Asp	Ala	Leu	Lys	Ala	Leu	His	Lys	Ala	Gly	Ile	Gln	Ala	Ile	Ala
	995					1000						1005			
Asp	Trp	Val	Pro	Asp	Gln	Ile	Tyr	Gln	Leu	Pro	Gly	Lys	Glu	Val	
1010						1015					1020				
Val	Thr	Ala	Thr	Arg	Thr	Asp	Gly	Ala	Gly	Arg	Lys	Ile	Ala	Asp	
1025					1030						1035				
Ala	Ile	Ile	Asp	His	Ser	Leu	Tyr	Val	Ala	Asn	Ser	Lys	Ser	Ser	
1040					1045						1050				
Gly	Arg	Asp	Tyr	Gln	Ala	Gln	Tyr	Gly	Gly	Glu	Phe	Leu	Ala	Glu	
1055					1060						1065				
Leu	Lys	Ala	Lys	Tyr	Pro	Lys	Met	Phe	Thr	Glu	Asn	Met	Ile	Ser	
1070					1075						1080				
Thr	Gly	Lys	Pro	Ile	Asp	Asp	Ser	Val	Lys	Leu	Lys	Gln	Trp	Lys	
1085					1090						1095				
Ala	Lys	Tyr	Phe	Asn	Gly	Thr	Asn	Val	Leu	Asp	Arg	Gly	Val	Gly	
1100					1105						1110				
Tyr	Val	Leu	Ser	Asp	Glu	Ala	Thr	Gly	Lys	Tyr	Phe	Thr	Val	Thr	
1115					1120						1125				
Lys	Glu	Gly	Asn	Phe	Ile	Pro	Leu	Gln	Leu	Thr	Gly	Asn	Glu	Lys	
1130					1135						1140				
Ala	Val	Thr	Gly	Phe	Ser	Asn	Asp	Gly	Lys	Gly	Ile	Thr	Tyr	Phe	
1145					1150						1155				
Gly	Thr	Ser	Gly	Asn	Gln	Ala	Lys	Ser	Ala	Phe	Val	Thr	Phe	Asn	
1160					1165						1170				
Gly	Asn	Thr	Tyr	Tyr	Phe	Asp	Ala	Arg	Gly	His	Met	Val	Thr	Asn	
1175					1180						1185				
Gly	Glu	Tyr	Ser	Pro	Asn	Gly	Lys	Asp	Val	Tyr	Arg	Phe	Leu	Pro	
1190					1195						1200				
Asn	Gly	Ile	Met	Leu	Ser	Asn	Ala	Phe	Tyr	Val	Asp	Ala	Asn	Gly	
1205					1210						1215				
Asn	Thr	Tyr	Leu	Tyr	Asn	Tyr	Lys	Gly	Gln	Met	Tyr	Lys	Gly	Gly	
1220					1225						1230				

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<210> SEQ ID NO 62
<211> LENGTH: 1518
<212> TYPE: PRT
<213> ORGANISM: Streptococcus salivarius SK126

<400> SEQUENCE: 62

Met Glu Asn Lys Ile His Tyr Lys Leu His Lys Val Lys Lys Gln Trp
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Val Thr Ile Ala Val Ala Ser Val Ala Leu Ala Thr Val Leu Gly Gly
          20             25             30
Leu Ser Val Thr Thr Ser Ser Val Ser Ala Asp Glu Thr Gln Asp Lys

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	35					40					45				
Thr	Val	Thr	Gln	Ser	Asn	Ser	Gly	Thr	Thr	Ala	Ser	Leu	Val	Thr	Ser
50						55					60				
Pro	Glu	Ala	Thr	Lys	Glu	Ala	Asp	Lys	Arg	Thr	Asn	Thr	Lys	Glu	Ala
65					70				75					80	
Asp	Val	Leu	Thr	Pro	Ala	Lys	Glu	Thr	Asn	Ala	Val	Glu	Thr	Ala	Thr
				85					90					95	
Thr	Thr	Asn	Thr	Gln	Ala	Thr	Ala	Glu	Ala	Ala	Thr	Thr	Ala	Thr	Thr
		100						105					110		
Ala	Asp	Val	Ala	Val	Ala	Ala	Val	Pro	Asn	Lys	Glu	Ala	Val	Val	Thr
		115					120					125			
Thr	Asp	Ala	Pro	Ala	Val	Thr	Thr	Glu	Lys	Ala	Glu	Glu	Gln	Pro	Ala
	130					135					140				
Thr	Val	Lys	Ala	Glu	Val	Val	Asn	Thr	Glu	Val	Lys	Ala	Pro	Glu	Ala
145					150					155				160	
Ala	Leu	Lys	Asp	Ser	Glu	Val	Glu	Ala	Ala	Leu	Ser	Leu	Lys	Asn	Ile
				165				170						175	
Lys	Asn	Ile	Asp	Gly	Lys	Tyr	Tyr	Tyr	Val	Asn	Glu	Asp	Gly	Ser	His
			180					185					190		
Lys	Glu	Asn	Phe	Ala	Ile	Thr	Val	Asn	Gly	Gln	Leu	Leu	Tyr	Phe	Gly
		195					200					205			
Lys	Asp	Gly	Ala	Leu	Thr	Ser	Ser	Ser	Thr	Tyr	Ser	Phe	Thr	Pro	Gly
	210					215					220				
Thr	Thr	Asn	Ile	Val	Asp	Gly	Phe	Ser	Ile	Asn	Asn	Arg	Ala	Tyr	Asp
225					230					235				240	
Ser	Ser	Glu	Ala	Ser	Phe	Glu	Leu	Ile	Asp	Gly	Tyr	Leu	Thr	Ala	Asp
				245					250					255	
Ser	Trp	Tyr	Arg	Pro	Ala	Ser	Ile	Ile	Lys	Asp	Gly	Val	Thr	Trp	Gln
			260					265					270		
Ala	Ser	Thr	Ala	Glu	Asp	Phe	Arg	Pro	Leu	Leu	Met	Ala	Trp	Trp	Pro
		275					280					285			
Asn	Val	Asp	Thr	Gln	Val	Asn	Tyr	Leu	Asn	Tyr	Met	Ser	Lys	Val	Phe
	290					295					300				
Asn	Leu	Asp	Ala	Lys	Tyr	Ser	Ser	Thr	Asp	Lys	Gln	Glu	Thr	Leu	Lys
305					310					315				320	
Val	Ala	Ala	Lys	Asp	Ile	Gln	Ile	Lys	Ile	Glu	Gln	Lys	Ile	Gln	Ala
				325					330					335	
Glu	Lys	Ser	Thr	Gln	Trp	Leu	Arg	Glu	Thr	Ile	Ser	Ala	Phe	Val	Lys
			340					345					350		
Thr	Gln	Pro	Gln	Trp	Asn	Lys	Glu	Thr	Glu	Asn	Tyr	Ser	Lys	Gly	Gly
		355					360					365			
Gly	Glu	Asp	His	Leu	Gln	Gly	Gly	Ala	Leu	Leu	Tyr	Val	Asn	Asp	Ser
	370					375					380				
Arg	Thr	Pro	Trp	Ala	Asn	Ser	Asp	Tyr	Arg	Arg	Leu	Asn	Arg	Thr	Ala
385					390					395				400	
Thr	Asn	Gln	Thr	Gly	Thr	Ile	Asp	Lys	Ser	Ile	Leu	Asp	Glu	Gln	Ser
				405					410					415	
Asp	Pro	Asn	His	Met	Gly	Gly	Phe	Asp	Phe	Leu	Leu	Ala	Asn	Asp	Val
			420					425					430		
Asp	Leu	Ser	Asn	Pro	Val	Val	Gln	Ala	Glu	Gln	Leu	Asn	Gln	Ile	His
	435						440					445			

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Tyr	Leu	Met	Asn	Trp	Gly	Ser	Ile	Val	Met	Gly	Asp	Lys	Asp	Ala	Asn	
450						455					460					
Phe	Asp	Gly	Ile	Arg	Val	Asp	Ala	Val	Asp	Asn	Val	Asp	Ala	Asp	Met	
465					470					475					480	
Leu	Gln	Leu	Tyr	Thr	Asn	Tyr	Phe	Arg	Glu	Tyr	Tyr	Gly	Val	Asn	Lys	
				485					490					495		
Ser	Glu	Ala	Asn	Ala	Leu	Ala	His	Ile	Ser	Val	Leu	Glu	Ala	Trp	Ser	
			500					505					510			
Leu	Asn	Asp	Asn	His	Tyr	Asn	Asp	Lys	Thr	Asp	Gly	Ala	Ala	Leu	Ala	
		515					520					525				
Met	Glu	Asn	Lys	Gln	Arg	Leu	Ala	Leu	Leu	Phe	Ser	Leu	Ala	Lys	Pro	
	530					535					540					
Ile	Lys	Glu	Arg	Thr	Pro	Ala	Val	Ser	Pro	Leu	Tyr	Asn	Asn	Thr	Phe	
545					550					555					560	
Asn	Thr	Thr	Gln	Arg	Asp	Glu	Lys	Thr	Asp	Trp	Ile	Asn	Lys	Asp	Gly	
				565					570					575		
Ser	Lys	Ala	Tyr	Asn	Glu	Asp	Gly	Thr	Val	Lys	Gln	Ser	Thr	Ile	Gly	
			580					585					590			
Lys	Tyr	Asn	Glu	Lys	Tyr	Gly	Asp	Ala	Ser	Gly	Asn	Tyr	Val	Phe	Ile	
		595					600					605				
Arg	Ala	His	Asp	Asn	Asn	Val	Gln	Asp	Ile	Ile	Ala	Glu	Ile	Ile	Lys	
	610					615					620					
Lys	Glu	Ile	Asn	Pro	Lys	Ser	Asp	Gly	Phe	Thr	Ile	Thr	Asp	Ala	Glu	
625					630					635					640	
Met	Lys	Gln	Ala	Phe	Glu	Ile	Tyr	Asn	Lys	Asp	Met	Leu	Ser	Ser	Asp	
			645						650					655		
Lys	Lys	Tyr	Thr	Leu	Asn	Asn	Ile	Pro	Ala	Ala	Tyr	Ala	Val	Met	Leu	
			660					665					670			
Gln	Asn	Met	Glu	Thr	Ile	Thr	Arg	Val	Tyr	Tyr	Gly	Asp	Leu	Tyr	Thr	
		675					680					685				
Asp	Asp	Gly	His	Tyr	Met	Glu	Thr	Lys	Ser	Pro	Tyr	Tyr	Asp	Thr	Ile	
	690					695					700					
Val	Asn	Leu	Met	Lys	Ser	Arg	Ile	Lys	Tyr	Val	Ser	Gly	Gly	Gln	Ala	
705					710					715					720	
Gln	Arg	Ser	Tyr	Trp	Leu	Pro	Thr	Asp	Gly	Lys	Met	Asp	Asn	Ser	Asp	
				725					730					735		
Val	Glu	Leu	Tyr	Arg	Thr	Asn	Glu	Val	Tyr	Thr	Ser	Val	Arg	Tyr	Gly	
			740					745					750			
Lys	Asp	Ile	Met	Thr	Ala	Asn	Asp	Thr	Glu	Gly	Ser	Lys	Tyr	Ser	Arg	
		755					760					765				
Thr	Ser	Gly	Gln	Val	Thr	Leu	Val	Ala	Asn	Asn	Pro	Lys	Leu	Thr	Leu	
		770				775					780					
Asp	Gln	Ser	Ala	Lys	Leu	Asn	Val	Glu	Met	Gly	Lys	Ile	His	Ala	Asn	
785					790					795					800	
Gln	Lys	Tyr	Arg	Ala	Leu	Ile	Val	Gly	Thr	Ala	Asp	Gly	Ile	Lys	Asn	
				805					810					815		
Phe	Thr	Ser	Asp	Ala	Asp	Ala	Ile	Ala	Ala	Gly	Tyr	Val	Lys	Glu	Thr	
			820					825					830			
Asp	Ser	Asn	Gly	Val	Leu	Thr	Phe	Gly	Ala	Asn	Asp	Ile	Lys	Gly	Tyr	
		835					840					845				

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Glu	Thr	Phe	Asp	Met	Ser	Gly	Phe	Val	Ala	Val	Trp	Val	Pro	Val	Gly	850	855	860
Ala	Ser	Asp	Asp	Gln	Asp	Ile	Arg	Val	Ala	Pro	Ser	Thr	Glu	Ala	Lys	865	870	875
Lys	Glu	Gly	Glu	Leu	Thr	Leu	Lys	Ala	Thr	Glu	Ala	Tyr	Asp	Ser	Gln	885	890	895
Leu	Ile	Tyr	Glu	Gly	Phe	Ser	Asn	Phe	Gln	Thr	Ile	Pro	Asp	Gly	Ser	900	905	910
Asp	Pro	Ser	Val	Tyr	Thr	Asn	Arg	Lys	Ile	Ala	Glu	Asn	Val	Asp	Leu	915	920	925
Phe	Lys	Ser	Trp	Gly	Val	Thr	Ser	Phe	Glu	Met	Ala	Pro	Gln	Phe	Val	930	935	940
Ser	Ala	Asp	Asp	Gly	Thr	Phe	Leu	Asp	Ser	Val	Ile	Gln	Asn	Gly	Tyr	945	950	955
Ala	Phe	Ala	Asp	Arg	Tyr	Asp	Leu	Ala	Met	Ser	Lys	Asn	Asn	Lys	Tyr	965	970	975
Gly	Ser	Lys	Glu	Asp	Leu	Arg	Asp	Ala	Leu	Lys	Ala	Leu	His	Lys	Ala	980	985	990
Gly	Ile	Gln	Ala	Ile	Ala	Asp	Trp	Val	Pro	Asp	Gln	Ile	Tyr	Gln	Leu	995	1000	1005
Pro	Gly	Lys	Glu	Val	Val	Thr	Ala	Thr	Arg	Thr	Asp	Gly	Ala	Gly		1010	1015	1020
Arg	Lys	Ile	Ala	Asp	Ala	Ile	Ile	Asp	His	Ser	Leu	Tyr	Val	Ala		1025	1030	1035
Asn	Thr	Lys	Ser	Ser	Gly	Lys	Asp	Tyr	Gln	Ala	Lys	Tyr	Gly	Gly		1040	1045	1050
Glu	Phe	Leu	Ala	Glu	Leu	Lys	Ala	Lys	Tyr	Pro	Glu	Met	Phe	Lys		1055	1060	1065
Val	Asn	Met	Ile	Ser	Thr	Gly	Lys	Pro	Ile	Asp	Asp	Ser	Val	Lys		1070	1075	1080
Leu	Lys	Gln	Trp	Lys	Ala	Glu	Tyr	Phe	Asn	Gly	Thr	Asn	Val	Leu		1085	1090	1095
Glu	Arg	Gly	Val	Gly	Tyr	Val	Leu	Ser	Asp	Glu	Ala	Thr	Gly	Lys		1100	1105	1110
Tyr	Phe	Thr	Val	Thr	Lys	Asp	Gly	Asn	Phe	Ile	Pro	Leu	Gln	Leu		1115	1120	1125
Thr	Gly	Asn	Glu	Lys	Val	Val	Thr	Gly	Phe	Ser	Asn	Asp	Gly	Lys		1130	1135	1140
Gly	Ile	Thr	Tyr	Phe	Gly	Thr	Ser	Gly	Thr	Gln	Ala	Lys	Ser	Ala		1145	1150	1155
Phe	Val	Thr	Phe	Asn	Gly	Asn	Thr	Tyr	Tyr	Phe	Asp	Ala	Arg	Gly		1160	1165	1170
His	Met	Val	Thr	Asn	Gly	Glu	Tyr	Ser	Pro	Asn	Gly	Lys	Asp	Val		1175	1180	1185
Tyr	Arg	Phe	Leu	Pro	Asn	Gly	Ile	Met	Leu	Ser	Asn	Ala	Phe	Tyr		1190	1195	1200
Val	Asp	Ala	Asn	Gly	Asn	Thr	Tyr	Leu	Tyr	Asn	Ser	Lys	Gly	Gln		1205	1210	1215
Met	Tyr	Lys	Gly	Gly	Tyr	Thr	Lys	Phe	Asp	Val	Thr	Glu	Thr	Asp		1220	1225	1230
Lys	Asp	Gly	Lys	Glu	Ser	Lys	Val	Val	Lys	Phe	Arg	Tyr	Phe	Thr				

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<210> SEQ ID NO 63
<211> LENGTH: 1431
<212> TYPE: PRT
<213> ORGANISM: Streptococcus salivarius PS4

<400> SEQUENCE: 63

Met Thr Lys Glu Thr Asn Thr Val Asp Ala Ala Thr Thr Thr Asn Thr
1          5          10          15
Gln Ala Ala Ala Asp Ala Ala Thr Lys Thr Ala Asp Ala Ala Val Thr
          20          25          30
Ala Leu Pro Asn Lys Glu Ala Val Thr Thr Asp Ala Pro Ala Val
          35          40          45
Thr Thr Glu Lys Ala Ala Glu Gln Pro Ala Thr Val Lys Ser Glu Val
          50          55          60

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Val 65	Asn	Thr	Glu	Val	Lys 70	Ala	Pro	Glu	Ala	Ala 75	Leu	Lys	Asp	Ser	Glu 80
Val	Glu	Ala	Ala	Leu	Ser	Leu	Lys	Asn	Ile	Lys	Asn	Ile	Asp	Gly	Lys 95
Tyr	Tyr	Tyr	Val	Asn	Lys	Asp	Gly	Ser	His	Lys	Glu	Asn	Phe	Ala	Ile 110
Thr	Val	Asn	Gly	Gln	Leu	Leu	Tyr	Phe	Gly	Lys	Asp	Gly	Ala	Leu	Thr 125
Ser	Ser	Ser	Thr	Tyr	Ser	Phe	Thr	Gln	Gly	Thr	Thr	Asn	Ile	Val	Asp 140
Gly	Phe	Ser	Lys	Asn	Asn	Arg	Ala	Tyr	Asp	Ser	Ser	Glu	Ala	Ser	Phe 160
Glu	Leu	Ile	Asp	Gly	Tyr	Leu	Thr	Ala	Asp	Ser	Trp	Tyr	Arg	Pro	Val 175
Ser	Ile	Ile	Lys	Asp	Gly	Val	Thr	Trp	Gln	Ala	Ser	Thr	Lys	Glu	Asp 190
Phe	Arg	Pro	Leu	Leu	Met	Ala	Trp	Trp	Pro	Asn	Val	Asp	Thr	Gln	Val 205
Asn	Tyr	Leu	Asn	Tyr	Met	Ser	Lys	Val	Phe	Asn	Leu	Asp	Ala	Lys	Tyr 220
Thr	Ser	Thr	Asp	Lys	Gln	Val	Asp	Leu	Asn	Arg	Ala	Ala	Lys	Asp	Ile 240
Gln	Val	Lys	Ile	Glu	Gln	Lys	Ile	Gln	Ala	Glu	Lys	Ser	Thr	Gln	Trp 255
Leu	Arg	Glu	Ala	Ile	Ser	Ala	Phe	Val	Lys	Thr	Gln	Pro	Gln	Trp	Asn 270
Lys	Glu	Thr	Glu	Asn	Phe	Ser	Lys	Gly	Gly	Gly	Glu	Asp	His	Leu	Gln 285
Gly	Gly	Ala	Leu	Leu	Tyr	Val	Asn	Asp	Pro	Arg	Thr	Pro	Trp	Ala	Asn 300
Ser	Asn	Tyr	Arg	Leu	Leu	Asn	Arg	Thr	Ala	Thr	Asn	Gln	Thr	Gly	Thr 320
Ile	Asp	Lys	Ser	Val	Leu	Asp	Glu	Gln	Ser	Asp	Pro	Asn	His	Met	Gly 335
Gly	Phe	Asp	Phe	Leu	Leu	Ala	Asn	Asp	Val	Asp	Thr	Ser	Asn	Pro	Val 350
Val	Gln	Ala	Glu	Gln	Leu	Asn	Gln	Ile	His	Tyr	Leu	Met	Asn	Trp	Gly 365
Ser	Ile	Val	Met	Gly	Asp	Lys	Asp	Ala	Asn	Phe	Asp	Gly	Ile	Arg	Val 380
Asp	Ala	Val	Asp	Asn	Val	Asp	Ala	Asp	Met	Leu	Gln	Leu	Tyr	Thr	Asn 400
Tyr	Phe	Arg	Glu	Tyr	Tyr	Gly	Val	Asn	Lys	Ser	Glu	Ala	Asn	Ala	Leu 415
Ala	His	Ile	Ser	Val	Leu	Glu	Ala	Trp	Ser	Leu	Asn	Asp	Asn	His	Tyr 430
Asn	Asp	Lys	Thr	Asp	Gly	Ala	Ala	Leu	Ala	Met	Glu	Asn	Lys	Gln	Arg 445
Leu	Ala	Leu	Leu	Phe	Ser	Leu	Ala	Lys	Pro	Ile	Lys	Glu	Arg	Thr	Pro 460
Ala	Val	Ser	Pro	Leu	Tyr	Asn	Asn	Thr	Phe	Asn	Thr	Thr	Gln	Arg	Asp

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465	470	475	480
Glu Lys Thr Asp Trp Ile Asn Lys Asp Gly Ser Lys Ala Tyr Asn Glu			
	485	490	495
Asp Gly Thr Val Lys Gln Ser Thr Ile Gly Lys Tyr Asn Glu Lys Tyr			
	500	505	510
Gly Asp Ala Ser Gly Asn Tyr Val Phe Ile Arg Ala His Asp Asn Asn			
	515	520	525
Val Gln Asp Ile Ile Ala Glu Ile Ile Lys Lys Glu Ile Asn Pro Lys			
	530	535	540
Ser Asp Gly Phe Thr Ile Thr Asp Ala Glu Met Lys Lys Ala Phe Glu			
	545	550	555
Ile Tyr Asn Lys Asp Met Leu Ser Ser Asp Lys Lys Tyr Thr Leu Asn			
	565	570	575
Asn Ile Pro Ala Ala Tyr Ala Val Met Leu Gln Asn Met Glu Thr Ile			
	580	585	590
Thr Arg Val Tyr Tyr Gly Asp Leu Tyr Thr Asp Asp Gly His Tyr Met			
	595	600	605
Glu Thr Lys Ser Pro Tyr Tyr Asp Thr Ile Val Asn Leu Met Lys Asn			
	610	615	620
Arg Ile Lys Tyr Val Ser Gly Gly Gln Ala Gln Arg Ser Tyr Trp Leu			
	625	630	635
Pro Thr Asp Gly Lys Met Asp Lys Ser Asp Val Glu Leu Tyr Arg Thr			
	645	650	655
Asn Glu Val Tyr Thr Ser Val Arg Tyr Gly Lys Asp Ile Met Thr Ala			
	660	665	670
Asp Asp Thr Gln Gly Ser Lys Tyr Ser Arg Thr Ser Gly Gln Val Thr			
	675	680	685
Leu Val Val Asn Asn Pro Lys Leu Ser Leu Asp Lys Ser Ala Lys Leu			
	690	695	700
Asp Val Glu Met Gly Lys Ile His Ala Asn Gln Lys Tyr Arg Ala Leu			
	705	710	715
Ile Val Gly Thr Pro Asn Gly Ile Lys Asn Phe Thr Ser Asp Ala Glu			
	725	730	735
Ala Ile Ala Ala Gly Tyr Val Lys Glu Thr Asp Gly Asn Gly Val Leu			
	740	745	750
Thr Phe Gly Ala Asn Asp Ile Lys Gly Tyr Glu Thr Phe Asp Met Ser			
	755	760	765
Gly Phe Val Ala Val Trp Val Pro Val Gly Ala Ser Asp Asp Gln Asp			
	770	775	780
Ile Arg Val Ala Ala Ser Thr Ala Ala Lys Lys Glu Gly Glu Leu Thr			
	785	790	795
Leu Lys Ala Thr Glu Ala Tyr Asp Ser Gln Leu Ile Tyr Glu Gly Phe			
	805	810	815
Ser Asn Phe Gln Thr Ile Pro Asp Gly Ser Asp Pro Ser Val Tyr Thr			
	820	825	830
Asn Arg Lys Ile Ala Glu Asn Val Asp Leu Phe Lys Ser Trp Gly Val			
	835	840	845
Thr Ser Phe Glu Met Ala Pro Gln Phe Val Ser Ala Asp Asp Gly Thr			
	850	855	860
Phe Leu Asp Ser Val Ile Gln Asn Gly Tyr Ala Phe Ala Asp Arg Tyr			
	865	870	875
			880

Asp	Leu	Ala	Met	Ser	Lys	Asn	Asn	Lys	Tyr	Gly	Ser	Lys	Glu	Asp	Leu
				885				890				895			
Arg	Asn	Ala	Leu	Lys	Ala	Leu	His	Lys	Ala	Gly	Ile	Gln	Ala	Ile	Ala
				900				905				910			
Asp	Trp	Val	Pro	Asp	Gln	Ile	Tyr	Gln	Leu	Pro	Gly	Lys	Glu	Val	Val
				915				920				925			
Thr	Ala	Thr	Arg	Thr	Asp	Gly	Ala	Gly	Arg	Lys	Ile	Ser	Asp	Ala	Ile
				930				935				940			
Ile	Asp	His	Ser	Leu	Tyr	Val	Ala	Asn	Ser	Lys	Ser	Ser	Gly	Lys	Asp
				945				950				955			
Tyr	Gln	Ala	Lys	Tyr	Gly	Gly	Glu	Phe	Leu	Ala	Glu	Leu	Lys	Ala	Lys
				965				970				975			
Tyr	Pro	Glu	Met	Phe	Lys	Val	Asn	Met	Ile	Ser	Thr	Gly	Lys	Pro	Ile
				980				985				990			
Asp	Asp	Ser	Val	Lys	Leu	Lys	Gln	Trp	Lys	Ala	Glu	Tyr	Phe	Asn	Gly
				995				1000				1005			
Thr	Asn	Val	Leu	Asp	Arg	Gly	Val	Gly	Tyr	Val	Leu	Ser	Asp	Glu	
				1010				1015				1020			
Ala	Thr	Gly	Lys	Tyr	Phe	Thr	Val	Thr	Lys	Glu	Gly	Asn	Phe	Ile	
				1025				1030				1035			
Pro	Leu	Gln	Leu	Lys	Gly	Asn	Glu	Lys	Val	Ile	Thr	Gly	Phe	Ser	
				1040				1045				1050			
Ser	Asp	Gly	Lys	Gly	Ile	Thr	Tyr	Phe	Gly	Thr	Ser	Gly	Asn	Gln	
				1055				1060				1065			
Ala	Lys	Ser	Ala	Phe	Val	Thr	Phe	Asn	Gly	Asn	Thr	Tyr	Tyr	Phe	
				1070				1075				1080			
Asp	Ala	Arg	Gly	His	Met	Val	Thr	Asn	Gly	Glu	Tyr	Ser	Pro	Asn	
				1085				1090				1095			
Gly	Lys	Asp	Val	Tyr	Arg	Phe	Leu	Pro	Asn	Gly	Ile	Met	Leu	Ser	
				1100				1105				1110			
Asn	Ala	Phe	Tyr	Val	Asp	Gly	Asn	Gly	Asn	Thr	Tyr	Leu	Tyr	Asn	
				1115				1120				1125			
Ser	Lys	Gly	Gln	Met	Tyr	Lys	Gly	Gly	Tyr	Ser	Lys	Phe	Asp	Val	
				1130				1135				1140			
Thr	Glu	Thr	Lys	Asp	Gly	Lys	Glu	Ser	Lys	Val	Val	Lys	Phe	Arg	
				1145				1150				1155			
Tyr	Phe	Thr	Asn	Glu	Gly	Val	Met	Ala	Lys	Gly	Val	Thr	Val	Val	
				1160				1165				1170			
Asp	Gly	Phe	Thr	Gln	Tyr	Phe	Asn	Glu	Asp	Gly	Ile	Gln	Ser	Lys	
				1175				1180				1185			
Asp	Glu	Leu	Val	Thr	Tyr	Asn	Gly	Lys	Thr	Tyr	Tyr	Phe	Glu	Ala	
				1190				1195				1200			
His	Thr	Gly	Asn	Ala	Ile	Lys	Asn	Thr	Trp	Arg	Asn	Ile	Lys	Gly	
				1205				1210				1215			
Lys	Trp	Tyr	His	Phe	Asp	Ala	Asn	Gly	Val	Ala	Ala	Thr	Gly	Ala	
				1220				1225				1230			
Gln	Val	Ile	Asn	Gly	Gln	His	Leu	Tyr	Phe	Asn	Glu	Asp	Gly	Ser	
				1235				1240				1245			
Gln	Val	Lys	Gly	Gly	Val	Val	Lys	Asn	Ala	Asp	Gly	Thr	Phe	Ser	
				1250				1255				1260			

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Lys	Tyr	Lys	Asp	Gly	Ser	Gly	Asp	Leu	Val	Val	Asn	Glu	Phe	Phe
1265						1270					1275			
Thr	Thr	Gly	Asp	Asn	Val	Trp	Tyr	Tyr	Ala	Gly	Ala	Asn	Gly	Lys
1280						1285					1290			
Thr	Val	Thr	Gly	Ala	Gln	Val	Ile	Asn	Gly	Gln	His	Leu	Phe	Phe
1295						1300					1305			
Lys	Glu	Asp	Gly	Ser	Gln	Val	Lys	Gly	Asp	Phe	Val	Lys	Asn	Ser
1310						1315					1320			
Asp	Gly	Thr	Tyr	Ser	Lys	Tyr	Asp	Ala	Ala	Ser	Gly	Glu	Arg	Leu
1325						1330					1335			
Thr	Asn	Glu	Phe	Phe	Thr	Thr	Gly	Asp	Asn	His	Trp	Tyr	Tyr	Ile
1340						1345					1350			
Gly	Ala	Asn	Gly	Lys	Thr	Val	Thr	Gly	Glu	Val	Lys	Ile	Gly	Asp
1355						1360					1365			
Asp	Thr	Tyr	Phe	Phe	Ala	Lys	Asp	Gly	Lys	Gln	Leu	Lys	Gly	Gln
1370						1375					1380			
Ile	Val	Thr	Thr	Arg	Ser	Gly	Arg	Ile	Ser	Tyr	Tyr	Phe	Gly	Asp
1385						1390					1395			
Ser	Gly	Lys	Lys	Ala	Ile	Ser	Thr	Trp	Val	Glu	Ile	Gln	Pro	Gly
1400						1405					1410			
Val	Phe	Val	Phe	Phe	Asp	Lys	Asn	Gly	Leu	Ala	Tyr	Pro	Pro	Glu
1415						1420					1425			
Asn	Met	Asn												
1430														

<210> SEQ ID NO 64
 <211> LENGTH: 1532
 <212> TYPE: PRT
 <213> ORGANISM: unknown
 <220> FEATURE:
 <223> OTHER INFORMATION: unknown Streptococcus sp. C150

<400> SEQUENCE: 64

Met	Glu	Asn	Lys	Val	His	Tyr	Lys	Leu	His	Lys	Val	Lys	Lys	Gln	Trp
1			5					10						15	
Val	Thr	Ile	Ala	Val	Ala	Ser	Ala	Ala	Leu	Ala	Thr	Val	Val	Gly	Gly
		20						25					30		
Leu	Ser	Ala	Thr	Thr	Ser	Ser	Val	Ser	Ala	Asp	Glu	Thr	Gln	Asp	Lys
		35					40					45			
Thr	Val	Thr	Gln	Pro	Asn	Ser	Asp	Thr	Thr	Ala	Asp	Leu	Val	Thr	Ser
		50				55					60				
Thr	Glu	Ala	Thr	Lys	Glu	Val	Asp	Lys	Arg	Thr	Asn	Thr	Lys	Glu	Ala
65				70					75					80	
Asp	Val	Leu	Thr	Pro	Ala	Lys	Glu	Thr	Asn	Thr	Val	Glu	Thr	Ala	Ala
			85					90						95	
Thr	Thr	Asn	Thr	Gln	Ala	Thr	Ala	Glu	Ala	Ala	Lys	Thr	Ala	Thr	Thr
		100						105					110		
Thr	Asn	Thr	Gln	Ala	Thr	Ala	Glu	Val	Ala	Lys	Thr	Ala	Thr	Thr	Ala
		115					120					125			
Asp	Val	Ala	Val	Ala	Ala	Val	Pro	Asn	Lys	Glu	Ala	Val	Val	Thr	Thr
		130				135					140				
Asp	Ala	Pro	Ala	Val	Thr	Thr	Glu	Lys	Ala	Glu	Glu	Gln	Pro	Ala	Thr
145				150					155					160	

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Val	Lys	Ala	Glu	Val	Val	Asn	Thr	Glu	Val	Lys	Ala	Pro	Glu	Ala	Ala	
				165					170					175		
Leu	Lys	Asp	Ser	Glu	Val	Glu	Ala	Ala	Leu	Ser	Leu	Lys	Asn	Ile	Lys	
			180					185					190			
Asn	Ile	Asp	Gly	Lys	Tyr	Tyr	Tyr	Val	Asn	Glu	Asp	Gly	Ser	His	Lys	
		195					200					205				
Glu	Asn	Phe	Ala	Ile	Thr	Val	Asn	Gly	Gln	Leu	Leu	Tyr	Phe	Gly	Lys	
	210					215					220					
Asp	Gly	Ala	Leu	Thr	Ser	Ser	Ser	Thr	Tyr	Ser	Phe	Thr	Gln	Gly	Thr	
	225				230					235					240	
Thr	Asn	Ile	Val	Asp	Gly	Phe	Ser	Ile	Asn	Asn	Arg	Ala	Tyr	Asp	Ser	
			245						250					255		
Ser	Glu	Ala	Ser	Phe	Glu	Leu	Ile	Asp	Gly	Tyr	Leu	Thr	Ala	Asp	Ser	
			260					265					270			
Trp	Tyr	Arg	Pro	Ala	Ser	Ile	Ile	Lys	Asp	Gly	Val	Thr	Trp	Gln	Ala	
		275					280					285				
Ser	Thr	Ala	Glu	Asp	Phe	Arg	Pro	Leu	Leu	Met	Ala	Trp	Trp	Pro	Asn	
	290					295					300					
Val	Asp	Thr	Gln	Val	Asn	Tyr	Leu	Asn	Tyr	Met	Ser	Lys	Val	Phe	Asn	
	305				310					315					320	
Leu	Asp	Ala	Lys	Tyr	Ser	Ser	Thr	Asp	Lys	Gln	Glu	Thr	Leu	Lys	Val	
			325						330					335		
Ala	Ala	Lys	Asp	Ile	Gln	Ile	Lys	Ile	Glu	Gln	Lys	Ile	Gln	Ala	Glu	
			340					345					350			
Lys	Ser	Thr	Gln	Trp	Leu	Arg	Glu	Thr	Ile	Ser	Ala	Phe	Val	Lys	Thr	
		355					360					365				
Gln	Pro	Gln	Trp	Asn	Lys	Glu	Thr	Glu	Asn	Tyr	Ser	Lys	Gly	Gly	Gly	
	370					375					380					
Glu	Asp	His	Leu	Gln	Gly	Gly	Ala	Leu	Leu	Tyr	Val	Asn	Asp	Ser	Arg	
	385				390					395					400	
Thr	Pro	Trp	Ala	Asn	Ser	Asn	Tyr	Arg	Leu	Leu	Asn	Arg	Thr	Ala	Thr	
			405						410					415		
Asn	Gln	Thr	Gly	Thr	Ile	Asp	Lys	Ser	Ile	Leu	Asp	Glu	Gln	Ser	Asp	
			420					425					430			
Pro	Asn	His	Met	Gly	Gly	Phe	Asp	Phe	Leu	Leu	Ala	Asn	Asp	Val	Asp	
		435					440					445				
Leu	Ser	Asn	Pro	Val	Val	Gln	Ala	Glu	Gln	Leu	Asn	Gln	Ile	His	Tyr	
	450					455					460					
Leu	Met	Asn	Trp	Gly	Ser	Ile	Val	Met	Gly	Asp	Lys	Asp	Ala	Asn	Phe	
	465				470					475					480	
Asp	Gly	Ile	Arg	Val	Asp	Ala	Val	Asp	Asn	Val	Asp	Ala	Asp	Met	Leu	
			485						490					495		
Gln	Leu	Tyr	Thr	Asn	Tyr	Phe	Arg	Glu	Tyr	Tyr	Gly	Val	Asn	Lys	Ser	
		500						505					510			
Glu	Ala	Asn	Ala	Leu	Ala	His	Ile	Ser	Val	Leu	Glu	Ala	Trp	Ser	Leu	
		515					520					525				
Asn	Asp	Asn	His	Tyr	Asn	Asp	Lys	Thr	Asp	Val	Ala	Ala	Leu	Ala	Met	
	530					535					540					
Glu	Asn	Lys	Gln	Arg	Leu	Ala	Leu	Leu	Phe	Ser	Leu	Ala	Lys	Pro	Ile	
	545				550					555					560	
Lys	Glu	Arg	Thr	Pro	Ala	Val	Ser	Pro	Leu	Tyr	Asn	Asn	Thr	Phe	Asn	

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565							570							575						
Thr	Thr	Gln	Arg	Asp	Glu	Lys	Thr	Asp	Trp	Ile	Asn	Lys	Asp	Gly	Ser					
			580					585					590							
Lys	Ala	Tyr	Asn	Glu	Asp	Gly	Thr	Val	Lys	Lys	Ser	Thr	Ile	Gly	Lys					
		595					600					605								
Tyr	Asn	Glu	Lys	Tyr	Gly	Asp	Ala	Ser	Gly	Asn	Tyr	Val	Phe	Ile	Arg					
	610					615					620									
Ala	His	Asp	Asn	Asn	Val	Gln	Asp	Ile	Ile	Ala	Glu	Ile	Ile	Lys	Lys					
	625					630				635					640					
Glu	Ile	Asn	Glu	Lys	Ser	Asp	Gly	Phe	Thr	Ile	Thr	Asp	Ser	Glu	Met					
				645					650					655						
Lys	Arg	Ala	Phe	Glu	Ile	Tyr	Asn	Lys	Asp	Met	Leu	Ser	Asn	Asp	Lys					
		660						665					670							
Lys	Tyr	Thr	Leu	Asn	Asn	Ile	Pro	Ala	Ala	Tyr	Ala	Val	Met	Leu	Gln					
		675					680					685								
Asn	Met	Glu	Thr	Ile	Thr	Arg	Val	Tyr	Tyr	Gly	Asp	Leu	Tyr	Thr	Asp					
	690					695					700									
Asp	Gly	Asn	Tyr	Met	Glu	Ala	Lys	Ser	Pro	Tyr	Tyr	Asp	Thr	Ile	Val					
	705				710					715					720					
Asn	Leu	Met	Lys	Ser	Arg	Ile	Lys	Tyr	Val	Ser	Gly	Gly	Gln	Ala	Gln					
			725						730					735						
Arg	Ser	Tyr	Trp	Leu	Pro	Thr	Asp	Gly	Lys	Met	Asp	Lys	Ser	Asp	Val					
		740						745					750							
Glu	Leu	Tyr	Arg	Thr	Asn	Glu	Val	Tyr	Thr	Ser	Val	Arg	Tyr	Gly	Lys					
		755				760						765								
Asp	Ile	Met	Thr	Ala	Asp	Asp	Thr	Gln	Gly	Ser	Lys	Tyr	Ser	Arg	Thr					
	770					775					780									
Ser	Gly	Gln	Val	Thr	Leu	Val	Val	Asn	Asn	Pro	Lys	Leu	Thr	Leu	Asp					
	785				790					795					800					
Gln	Ser	Ala	Lys	Leu	Asn	Val	Val	Met	Gly	Lys	Ile	His	Ala	Asn	Gln					
			805						810					815						
Lys	Tyr	Arg	Ala	Leu	Ile	Val	Gly	Thr	Pro	Asn	Gly	Ile	Lys	Asn	Phe					
		820						825					830							
Thr	Ser	Asp	Ala	Glu	Ala	Ile	Ala	Ala	Gly	Tyr	Val	Lys	Glu	Thr	Asp					
		835				840						845								
Gly	Asn	Gly	Val	Leu	Thr	Phe	Gly	Ala	Asn	Asp	Ile	Lys	Gly	Tyr	Glu					
	850					855					860									
Thr	Phe	Asp	Met	Ser	Gly	Phe	Val	Ala	Val	Trp	Val	Pro	Val	Gly	Ala					
	865				870					875					880					
Ser	Asp	Asp	Gln	Asp	Ile	Arg	Val	Ala	Ala	Ser	Thr	Ala	Ala	Lys	Lys					
			885					890						895						
Glu	Gly	Glu	Leu	Thr	Leu	Lys	Ala	Thr	Glu	Ala	Tyr	Asp	Ser	Gln	Leu					
		900						905					910							
Ile	Tyr	Glu	Gly	Phe	Ser	Asn	Phe	Gln	Thr	Ile	Pro	Asp	Gly	Ser	Asp					
		915					920					925								
Pro	Ser	Val	Tyr	Thr	Asn	Arg	Lys	Ile	Ala	Glu	Asn	Val	Asp	Leu	Phe					
		930				935					940									
Lys	Ser	Trp	Gly	Val	Thr	Ser	Phe	Glu	Met	Ala	Pro	Gln	Phe	Val	Ser					
	945					950				955					960					
Ala	Asp	Asp	Gly	Thr	Phe	Leu	Asp	Ser	Val	Ile	Gln	Asn	Gly	Tyr	Ala					
			965					970						975						

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Phe	Ala	Asp	Arg	Tyr	Asp	Leu	Ala	Met	Ser	Lys	Asn	Asn	Lys	Tyr	Gly
		980						985					990		
Ser	Lys	Glu	Asp	Leu	Arg	Asn	Ala	Leu	Lys	Ala	Leu	His	Lys	Ala	Gly
		995				1000						1005			
Ile	Gln	Ala	Ile	Ala	Asp	Trp	Val	Pro	Asp	Gln	Ile	Tyr	Gln	Leu	
	1010					1015						1020			
Pro	Gly	Lys	Glu	Val	Val	Thr	Ala	Thr	Arg	Thr	Asp	Gly	Ala	Gly	
	1025					1030						1035			
Arg	Lys	Ile	Ser	Asp	Ala	Ile	Ile	Asp	His	Ser	Leu	Tyr	Val	Ala	
	1040					1045						1050			
Asn	Ser	Lys	Ser	Ser	Gly	Lys	Asp	Tyr	Gln	Ala	Lys	Tyr	Gly	Gly	
	1055					1060						1065			
Glu	Phe	Leu	Ala	Glu	Leu	Lys	Ala	Lys	Tyr	Pro	Glu	Met	Phe	Lys	
	1070					1075						1080			
Val	Asn	Met	Ile	Ser	Thr	Gly	Lys	Pro	Ile	Asp	Asp	Ser	Val	Lys	
	1085					1090						1095			
Leu	Lys	Gln	Trp	Lys	Ala	Glu	Tyr	Phe	Asn	Gly	Thr	Asn	Val	Leu	
	1100					1105						1110			
Asp	Arg	Gly	Val	Gly	Tyr	Val	Leu	Ser	Asp	Glu	Ala	Thr	Gly	Lys	
	1115					1120						1125			
Tyr	Phe	Thr	Val	Thr	Lys	Glu	Gly	Asn	Phe	Ile	Pro	Leu	Gln	Leu	
	1130					1135						1140			
Lys	Gly	Asn	Lys	Lys	Val	Ile	Thr	Gly	Phe	Ser	Ser	Asp	Gly	Lys	
	1145					1150						1155			
Gly	Ile	Thr	Tyr	Phe	Gly	Thr	Ser	Gly	Asn	Gln	Ala	Lys	Ser	Ala	
	1160					1165						1170			
Phe	Val	Thr	Phe	Asn	Gly	Asn	Thr	Tyr	Tyr	Phe	Asp	Ala	Arg	Gly	
	1175					1180						1185			
His	Met	Val	Thr	Asn	Gly	Glu	Tyr	Ser	Pro	Asn	Gly	Lys	Asp	Val	
	1190					1195						1200			
Tyr	Arg	Phe	Leu	Pro	Asn	Gly	Ile	Met	Leu	Ser	Asn	Ala	Phe	Tyr	
	1205					1210						1215			
Val	Asp	Gly	Asn	Gly	Asn	Thr	Tyr	Leu	Tyr	Asn	Ser	Lys	Gly	Gln	
	1220					1225						1230			
Met	Tyr	Lys	Gly	Gly	Tyr	Ser	Lys	Phe	Asp	Val	Thr	Glu	Thr	Lys	
	1235					1240						1245			
Asp	Gly	Lys	Glu	Ser	Lys	Val	Val	Lys	Phe	Arg	Tyr	Phe	Thr	Asn	
	1250					1255						1260			
Glu	Gly	Val	Met	Ala	Lys	Gly	Val	Thr	Val	Val	Asp	Gly	Phe	Thr	
	1265					1270						1275			
Gln	Tyr	Phe	Asn	Glu	Asp	Gly	Ile	Gln	Ser	Lys	Asp	Glu	Leu	Val	
	1280					1285						1290			
Thr	Tyr	Asn	Gly	Lys	Thr	Tyr	Tyr	Phe	Glu	Ala	His	Thr	Gly	Asn	
	1295					1300						1305			
Ala	Ile	Lys	Asn	Thr	Trp	Arg	Asn	Ile	Lys	Gly	Lys	Trp	Tyr	His	
	1310					1315						1320			
Phe	Asp	Ala	Asn	Gly	Val	Ala	Ala	Thr	Gly	Ala	Gln	Val	Ile	Asn	
	1325					1330						1335			
Gly	Gln	His	Leu	Tyr	Phe	Asn	Glu	Asp	Gly	Ser	Gln	Val	Lys	Gly	
	1340					1345						1350			

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Ser	Ile	Val	Lys	Asn	Ala	Asp	Gly	Thr	Phe	Ser	Lys	Tyr	Lys	Asp
1355						1360					1365			
Ser	Ser	Gly	Asp	Leu	Val	Val	Asn	Glu	Phe	Phe	Thr	Thr	Gly	Asp
1370						1375					1380			
Asn	Val	Trp	Tyr	Tyr	Ala	Gly	Ala	Asn	Gly	Lys	Thr	Val	Thr	Gly
1385						1390					1395			
Ala	Gln	Val	Ile	Asn	Gly	Gln	His	Leu	Phe	Phe	Lys	Glu	Asp	Gly
1400						1405					1410			
Ser	Gln	Val	Lys	Gly	Asp	Phe	Val	Lys	Asn	Ser	Asp	Gly	Thr	Tyr
1415						1420					1425			
Ser	Lys	Tyr	Asp	Ala	Ala	Ser	Gly	Glu	Arg	Leu	Thr	Asn	Glu	Phe
1430						1435					1440			
Phe	Thr	Thr	Gly	Asp	Asn	His	Trp	Tyr	Tyr	Ile	Gly	Ala	Asn	Gly
1445						1450					1455			
Lys	Thr	Val	Thr	Gly	Glu	Val	Lys	Ile	Gly	Asp	Asp	Thr	Tyr	Phe
1460						1465					1470			
Phe	Ala	Lys	Asp	Gly	Lys	Gln	Leu	Lys	Gly	Gln	Ile	Val	Thr	Thr
1475						1480					1485			
Arg	Ser	Gly	Arg	Ile	Ser	Tyr	Tyr	Phe	Gly	Asp	Ser	Gly	Lys	Lys
1490						1495					1500			
Ala	Ile	Ser	Thr	Trp	Val	Glu	Ile	Gln	Pro	Gly	Val	Phe	Val	Phe
1505						1510					1515			
Phe	Asp	Lys	Asn	Gly	Leu	Ala	Tyr	Pro	Pro	Glu	Asn	Met	Asn	
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<210> SEQ ID NO 65

<211> LENGTH: 1341

<212> TYPE: PRT

<213> ORGANISM: Streptococcus salivarius

<400> SEQUENCE: 65

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Glu	Asn	Phe	Ala	Ile	Thr	Val	Asn	Gly	Gln	Leu	Leu	Tyr	Phe	Gly	Lys
		20						25					30		
Asp	Gly	Ala	Leu	Thr	Ser	Ser	Ser	Thr	Tyr	Ser	Phe	Thr	Pro	Gly	Thr
		35					40					45			
Thr	Asn	Ile	Val	Asp	Gly	Phe	Ser	Ile	Asn	Asn	Arg	Ala	Tyr	Asp	Ser
	50				55					60					
Ser	Glu	Ala	Ser	Phe	Glu	Leu	Ile	Asp	Gly	Tyr	Leu	Thr	Ala	Asp	Ser
65				70					75				80		
Trp	Tyr	Arg	Pro	Ala	Ser	Ile	Ile	Lys	Asp	Gly	Val	Thr	Trp	Gln	Ala
			85					90					95		
Ser	Thr	Ala	Glu	Asp	Phe	Arg	Pro	Leu	Leu	Met	Ala	Trp	Trp	Pro	Asn
		100						105					110		
Val	Asp	Thr	Gln	Val	Asn	Tyr	Leu	Asn	Tyr	Met	Ser	Lys	Val	Phe	Asn
		115					120					125			
Leu	Asp	Ala	Lys	Tyr	Ser	Ser	Thr	Asp	Lys	Gln	Glu	Thr	Leu	Lys	Val
	130					135					140				
Ala	Ala	Lys	Asp	Ile	Gln	Ile	Lys	Ile	Glu	Gln	Lys	Ile	Gln	Ala	Glu
145					150					155					160
Lys	Ser	Thr	Gln	Trp	Leu	Arg	Glu	Thr	Ile	Ser	Ala	Phe	Val	Lys	Thr
			165					170						175	

Gln	Pro	Gln	Trp	Asn	Lys	Glu	Thr	Glu	Asn	Tyr	Ser	Lys	Gly	Gly		
			180							185				190		
Glu	Asp	His	Leu	Gln	Gly	Gly	Ala	Leu	Leu	Tyr	Val	Asn	Asp	Ser	Arg	
			195				200							205		
Thr	Pro	Trp	Ala	Asn	Ser	Asp	Tyr	Arg	Arg	Leu	Asn	Arg	Thr	Ala	Thr	
			210				215							220		
Asn	Gln	Thr	Gly	Thr	Ile	Asp	Lys	Ser	Ile	Leu	Asp	Glu	Gln	Ser	Asp	
			225				230				235				240	
Pro	Asn	His	Met	Gly	Gly	Phe	Asp	Phe	Leu	Leu	Ala	Asn	Asp	Val	Asp	
			245							250				255		
Leu	Ser	Asn	Pro	Val	Val	Gln	Ala	Glu	Gln	Leu	Asn	Gln	Ile	His	Tyr	
			260							265				270		
Leu	Met	Asn	Trp	Gly	Ser	Ile	Val	Met	Gly	Asp	Lys	Asp	Ala	Asn	Phe	
			275				280							285		
Asp	Gly	Ile	Arg	Val	Asp	Ala	Val	Asp	Asn	Val	Asp	Ala	Asp	Met	Leu	
			290				295				300					
Gln	Leu	Tyr	Thr	Asn	Tyr	Phe	Arg	Glu	Tyr	Tyr	Gly	Val	Asn	Lys	Ser	
			305				310				315				320	
Glu	Ala	Asn	Ala	Leu	Ala	His	Ile	Ser	Val	Leu	Glu	Ala	Trp	Ser	Leu	
			325							330				335		
Asn	Asp	Asn	His	Tyr	Asn	Asp	Lys	Thr	Asp	Gly	Ala	Ala	Leu	Ala	Met	
			340							345				350		
Glu	Asn	Lys	Gln	Arg	Leu	Ala	Leu	Leu	Phe	Ser	Leu	Ala	Lys	Pro	Ile	
			355				360							365		
Lys	Glu	Arg	Thr	Pro	Ala	Val	Ser	Pro	Leu	Tyr	Asn	Asn	Thr	Phe	Asn	
			370				375				380					
Thr	Thr	Gln	Arg	Asp	Glu	Lys	Thr	Asp	Trp	Ile	Asn	Lys	Asp	Gly	Ser	
			385				390				395				400	
Lys	Ala	Tyr	Asn	Glu	Asp	Gly	Thr	Val	Lys	Gln	Ser	Thr	Ile	Gly	Lys	
			405							410				415		
Tyr	Asn	Glu	Lys	Tyr	Gly	Asp	Ala	Ser	Gly	Asn	Tyr	Val	Phe	Ile	Arg	
			420							425				430		
Ala	His	Asp	Asn	Asn	Val	Gln	Asp	Ile	Ile	Ala	Glu	Ile	Ile	Lys	Lys	
			435				440							445		
Glu	Ile	Asn	Pro	Lys	Ser	Asp	Gly	Phe	Thr	Ile	Thr	Asp	Ala	Glu	Met	
			450				455							460		
Lys	Gln	Ala	Phe	Glu	Ile	Tyr	Asn	Lys	Asp	Met	Leu	Ser	Ser	Asp	Lys	
			465				470				475				480	
Lys	Tyr	Thr	Leu	Asn	Asn	Ile	Pro	Ala	Ala	Tyr	Ala	Val	Met	Leu	Gln	
			485							490				495		
Asn	Met	Glu	Thr	Ile	Thr	Arg	Val	Tyr	Tyr	Gly	Asp	Leu	Tyr	Thr	Asp	
			500							505				510		
Asp	Gly	His	Tyr	Met	Glu	Thr	Lys	Ser	Pro	Tyr	Tyr	Asp	Thr	Ile	Val	
			515				520							525		
Asn	Leu	Met	Lys	Ser	Arg	Ile	Lys	Tyr	Val	Ser	Gly	Gly	Gln	Ala	Gln	
			530				535							540		
Arg	Ser	Tyr	Trp	Leu	Pro	Thr	Asp	Gly	Lys	Met	Asp	Asn	Ser	Asp	Val	
			545				550				555				560	
Glu	Leu	Tyr	Arg	Thr	Asn	Glu	Val	Tyr	Thr	Ser	Val</					

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Asp	Ile	Met	Thr	Ala	Asn	Asp	Thr	Glu	Gly	Ser	Lys	Tyr	Ser	Arg	Thr	580	585	590
Ser	Gly	Gln	Val	Thr	Leu	Val	Ala	Asn	Asn	Pro	Lys	Leu	Asn	Leu	Asp	595	600	605
Gln	Ser	Ala	Lys	Leu	Asn	Val	Glu	Met	Gly	Lys	Ile	His	Ala	Asn	Gln	610	615	620
Lys	Tyr	Arg	Ala	Leu	Ile	Val	Gly	Thr	Ala	Asp	Gly	Ile	Lys	Asn	Phe	625	630	635
Thr	Ser	Asp	Ala	Asp	Ala	Ile	Ala	Ala	Gly	Tyr	Val	Lys	Glu	Thr	Asp	645	650	655
Ser	Asn	Gly	Val	Leu	Thr	Phe	Gly	Ala	Asn	Asp	Ile	Lys	Gly	Tyr	Glu	660	665	670
Thr	Phe	Asp	Met	Ser	Gly	Phe	Val	Ala	Val	Trp	Val	Pro	Val	Gly	Ala	675	680	685
Ser	Asp	Asn	Gln	Asp	Ile	Arg	Val	Ala	Pro	Ser	Thr	Glu	Ala	Lys	Lys	690	695	700
Glu	Gly	Glu	Leu	Thr	Leu	Lys	Ala	Thr	Glu	Ala	Tyr	Asp	Ser	Gln	Leu	705	710	715
Ile	Tyr	Glu	Gly	Phe	Ser	Asn	Phe	Gln	Thr	Ile	Pro	Asp	Gly	Ser	Asp	725	730	735
Pro	Ser	Val	Tyr	Thr	Asn	Arg	Lys	Ile	Ala	Glu	Asn	Val	Asp	Leu	Phe	740	745	750
Lys	Ser	Trp	Gly	Val	Thr	Ser	Phe	Glu	Met	Ala	Pro	Gln	Phe	Val	Ser	755	760	765
Ala	Asp	Asp	Gly	Thr	Phe	Leu	Asp	Ser	Val	Ile	Gln	Asn	Gly	Tyr	Ala	770	775	780
Phe	Ala	Asp	Arg	Tyr	Asp	Leu	Ala	Met	Ser	Lys	Asn	Asn	Lys	Tyr	Gly	785	790	795
Ser	Lys	Glu	Asp	Leu	Arg	Asp	Ala	Leu	Lys	Ala	Leu	His	Lys	Ala	Gly	805	810	815
Ile	Gln	Ala	Ile	Ala	Asp	Trp	Val	Pro	Asp	Gln	Ile	Tyr	Gln	Leu	Pro	820	825	830
Gly	Lys	Glu	Val	Val	Thr	Ala	Thr	Arg	Thr	Asp	Gly	Ala	Gly	Arg	Lys	835	840	845
Ile	Ala	Asp	Ala	Ile	Ile	Asp	His	Ser	Leu	Tyr	Val	Ala	Asn	Ser	Lys	850	855	860
Ser	Ser	Gly	Lys	Asp	Tyr	Gln	Ala	Lys	Tyr	Gly	Gly	Glu	Phe	Leu	Ala	865	870	875
Glu	Leu	Lys	Ala	Lys	Tyr	Pro	Glu	Met	Phe	Lys	Val	Asn	Met	Ile	Ser	885	890	895
Thr	Gly	Lys	Pro	Ile	Asp	Asp	Ser	Val	Lys	Leu	Lys	Gln	Trp	Lys	Ala	900	905	910
Glu	Tyr	Phe	Asn	Gly	Thr	Asn	Val	Leu	Glu	Arg	Gly	Val	Gly	Tyr	Val	915	920	925
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Asn	Phe	Ile	Pro	Leu	Gln	Leu	Thr	Gly	Lys	Glu	Lys	Val	Ile	Thr	Gly	945	950	955
Phe	Ser	Ser	Asp	Gly	Lys	Gly	Ile	Thr	Tyr	Phe	Gly	Thr	Ser	Gly	Thr	965	970	975
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Asp	Lys	Leu	Val	Thr	Phe	Lys	Gly	Lys	Thr	Tyr	Tyr	Phe	Asp	Ala			
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Lys	Tyr	Lys	Glu	Gly	Phe	Gly	Glu	Leu	Val	Thr	Asn	Glu	Phe	Phe			
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Thr	Thr	Asp	Gly	Asn	Val	Trp	Tyr	Tyr	Ala	Gly	Ala	Asn	Gly	Lys			
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Thr	Val	Thr	Gly	Ala	Gln	Val	Ile	Asn	Gly	Gln	His	Leu	Tyr	Phe			
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Asn	Ala	Asp	Gly	Ser	Gln	Val	Lys	Gly	Gly	Val	Val	Lys	Asn	Ala			
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Gly	Ala	Asn	Gly	Lys	Ser	Val	Thr	Gly	Glu	Val	Lys	Ile	Gly	Asp			
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<211> LENGTH: 93

<212> TYPE: DNA

<213> ORGANISM: Unknown

<220> FEATURE:

<223> OTHER INFORMATION: terminator sequence added to pHYT

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What is claimed is:

1. A non-native glucosyltransferase comprising at least one amino acid substitution at a position corresponding with amino acid residue Asn-531, Arg-534, Thr-563, Glu-567, Val-586, Gln-588, Ile-591, Lys-593, Ile-608, Ala-610, Leu-661, Arg-722, Thr-728, Met-732, Arg-741, Asn-743, Ala-777, Tyr-848, or Ile-1453 of SEQ ID NO:62,

wherein the non-native glucosyltransferase synthesizes insoluble alpha-glucan comprising 1,3-linkages, and the molecular weight of said insoluble alpha-glucan is higher than the molecular weight of insoluble alpha-glucan synthesized by a second glucosyltransferase that only differs from the non-native glucosyltransferase at the substitution position(s).

2. The non-native glucosyltransferase of claim 1, wherein:

- (i) the amino acid substitution at the position corresponding with amino acid residue Asn-531 is with a Gly, Leu, or Met residue;
- (ii) the amino acid substitution at the position corresponding with amino acid residue Arg-534 is with a Lys, Gly, Ile, Leu, or Met residue;
- (iii) the amino acid substitution at the position corresponding with amino acid residue Thr-563 is with an Ala residue;
- (iv) the amino acid substitution at the position corresponding with amino acid residue Glu-567 is with a Gln residue;
- (v) the amino acid substitution at the position corresponding with amino acid residue Val-586 is with a Thr residue;
- (vi) the amino acid substitution at the position corresponding with amino acid residue Gln-588 is with a Leu residue;
- (vii) the amino acid substitution at the position corresponding with amino acid residue Ile-591 is with a Val, Lys, or Arg residue;
- (viii) the amino acid substitution at the position corresponding with amino acid residue Lys-593 is with a Met residue;
- (ix) the amino acid substitution at the position corresponding with amino acid residue Ile-608 is with a Tyr residue;
- (x) the amino acid substitution at the position corresponding with amino acid residue Ala-610 is with a Cys or Thr residue;

(xi) the amino acid substitution at the position corresponding with amino acid residue Leu-661 is with a Pro residue;

(xii) the amino acid substitution at the position corresponding with amino acid residue Arg-722 is with a His or Asn residue;

(xiii) the amino acid substitution at the position corresponding with amino acid residue Thr-728 is with a Ser residue;

(xiv) the amino acid substitution at the position corresponding with amino acid residue Met-732 is with a Leu residue;

(xv) the amino acid substitution at the position corresponding with amino acid residue Arg-741 is with a Ser, Ala, Pro, Gln, or Thr residue;

(xvi) the amino acid substitution at the position corresponding with amino acid residue Asn-743 is with a Ser, Thr, or Asp residue;

(xvii) the amino acid substitution at the position corresponding with amino acid residue Ala-777 is with an Asn residue;

(xviii) the amino acid substitution at the position corresponding with amino acid residue Tyr-848 is with a Glu residue; and/or

(xix) the amino acid substitution at the position corresponding with amino acid residue Ile-1453 is with a Gly or Met residue.

3. The non-native glucosyltransferase of claim 1, comprising at least one amino acid substitution at a position corresponding with amino acid residue Gln-588, Arg-741, or Arg-722 of SEQ ID NO:62; optionally wherein:

- (i) the amino acid substitution at the position corresponding with amino acid residue Gln-588 is with a Leu residue;
- (ii) the amino acid substitution at the position corresponding with amino acid residue Arg-741 is with a Ser residue; and/or
- (iii) the amino acid substitution at the position corresponding with amino acid residue Arg-722 is with a His residue.

4. The non-native glucosyltransferase of claim 3, comprising two or more amino acid substitutions at positions corresponding with amino acid residues Gln-588, Arg-741, or Arg-722 of SEQ ID NO:62.

5. The non-native glucosyltransferase of claim 1, wherein the insoluble alpha-glucan comprises at least about 50% alpha-1,3 linkages, and optionally wherein the insoluble alpha-glucan has a weight average degree of polymerization (DP_w) of at least 100.

6. The non-native glucosyltransferase of claim 5, wherein the insoluble alpha-glucan has a DP_w of at least 650.

7. The non-native glucosyltransferase of claim 6, comprising a catalytic domain that is at least about 90% identical to residues 55-960 of SEQ ID NO:4, residues 54-957 of SEQ ID NO:65, residues 55-960 of SEQ ID NO:30, residues 55-960 of SEQ ID NO:28, or residues 55-960 of SEQ ID NO:20.

8. The non-native glucosyltransferase of claim 7, comprising an amino acid sequence that is at least about 90% identical to SEQ ID NO:4, SEQ ID NO:65, SEQ ID NO:30, SEQ ID NO:28, or SEQ ID NO:20.

9. The non-native glucosyltransferase of claim 7, wherein the insoluble alpha-glucan comprises at least about 90% alpha-1,3 linkages.

10. The non-native glucosyltransferase of claim 1, wherein the molecular weight of said insoluble alpha-glucan is at least about 10% higher than the molecular weight of insoluble alpha-glucan synthesized by said second glucosyltransferase.

11. A polynucleotide comprising a nucleotide sequence encoding a non-native glucosyltransferase according to claim 1, optionally wherein one or more regulatory sequences are operably linked to the nucleotide sequence, and preferably wherein said one or more regulatory sequences include a promoter sequence.

12. A reaction composition comprising water, sucrose, and a non-native glucosyltransferase according to claim 1.

13. A method of producing insoluble alpha-glucan comprising:

- (a) contacting at least water, sucrose, and a non-native glucosyltransferase enzyme according to claim 1, whereby insoluble alpha-glucan is produced; and
- (b) optionally, isolating the insoluble alpha-glucan produced in step (a).

14. A method of preparing a polynucleotide sequence encoding a non-native glucosyltransferase, said method comprising:

- (a) identifying a polynucleotide sequence encoding a parent glucosyltransferase that (i) comprises an amino acid sequence that is at least about 40% identical to SEQ ID NO:4 or positions 55-960 of SEQ ID NO:4, and (ii) synthesizes insoluble alpha-glucan comprising 1,3-linkages; and
- (b) modifying the polynucleotide sequence identified in step (a) to substitute at least one amino acid of the parent glucosyltransferase at a position corresponding with amino acid residue Asn-531, Arg-534, Thr-563, Glu-567, Val-586, Gln-588, Ile-591, Lys-593, Ile-608, Ala-610, Leu-661, Arg-722, Thr-728, Met-732, Arg-741, Asn-743, Ala-777, Tyr-848, or Ile-1453 of SEQ ID NO:62,

thereby providing a polynucleotide sequence encoding a non-native glucosyltransferase that synthesizes insoluble alpha-glucan with a molecular weight that is higher than the molecular weight of insoluble alpha-glucan synthesized by the parent glucosyltransferase.

15. The method of claim 14, wherein said identifying step is performed:

- (a) in silico,
- (b) with a method comprising a nucleic acid hybridization step,
- (c) with a method comprising a protein sequencing step, and/or
- (d) with a method comprising a protein binding step; and/or wherein said modifying step is performed:
- (e) in silico, followed by synthesis of the polynucleotide sequence encoding the non-native glucosyltransferase enzyme, or
- (f) using a physical copy of the polynucleotide sequence encoding the parent glucosyltransferase.

* * * * *